

Network Systems
Science & Advanced
Computing
Biocomplexity Institute
& Initiative
University of Virginia

Analysis of COVID-19 in Virginia

June 9th, 2021

(data current to June 6th – June 8th)

Biocomplexity Institute Technical report: TR 2021-068



BIOCOMPLEXITY INSTITUTE

biocomplexity.virginia.edu

About Us

- Biocomplexity Institute at the University of Virginia
 - Using big data and simulations to understand massively interactive systems and solve societal problems
- Over 20 years of crafting and analyzing infectious disease models
 - Pandemic response for Influenza, Ebola, Zika, and others



Points of Contact

Bryan Lewis
brylew@virginia.edu

Srini Venkatramanan
srini@virginia.edu

Madhav Marathe
marathe@virginia.edu

Chris Barrett
ChrisBarrett@virginia.edu

Model Development, Outbreak Analytics, and Delivery Team

Przemyslaw Porebski, Joseph Outten, Brian Klahn, Alex Telionis,
Srinivasan Venkatramanan, Bryan Lewis,

Aniruddha Adiga, Hannah Baek, Chris Barrett, Jiangzhuo Chen, Patrick Corbett,
Stephen Eubank, Ben Hurt, Dustin Machi, Achla Marathe, Madhav Marathe, Mark Orr,
Akhil Peddireddy, Asal Pilehvari, Erin Raymond, James Schlitt, Anil Vullikanti, Lijing Wang,
James Walke, Andrew Warren, Amanda Wilson, Dawen Xie



Overview

- **Goal:** Understand impact of COVID-19 mitigations in Virginia
- **Approach:**
 - Calibrate explanatory mechanistic model to observed cases
 - Project based on scenarios for next 4 months
 - Consider a range of possible mitigation effects in "what-if" scenarios
- **Outcomes:**
 - Ill, Confirmed, Hospitalized, ICU, Ventilated, Death
 - Geographic spread over time, case counts, healthcare burdens

Key Takeaways

Projecting future cases precisely is impossible and unnecessary.

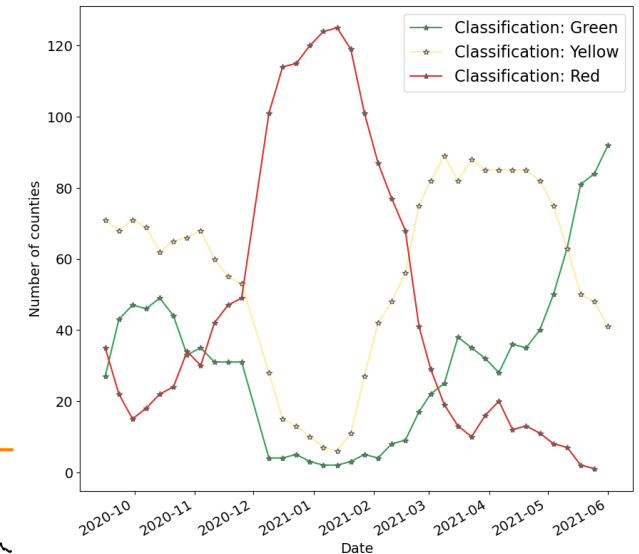
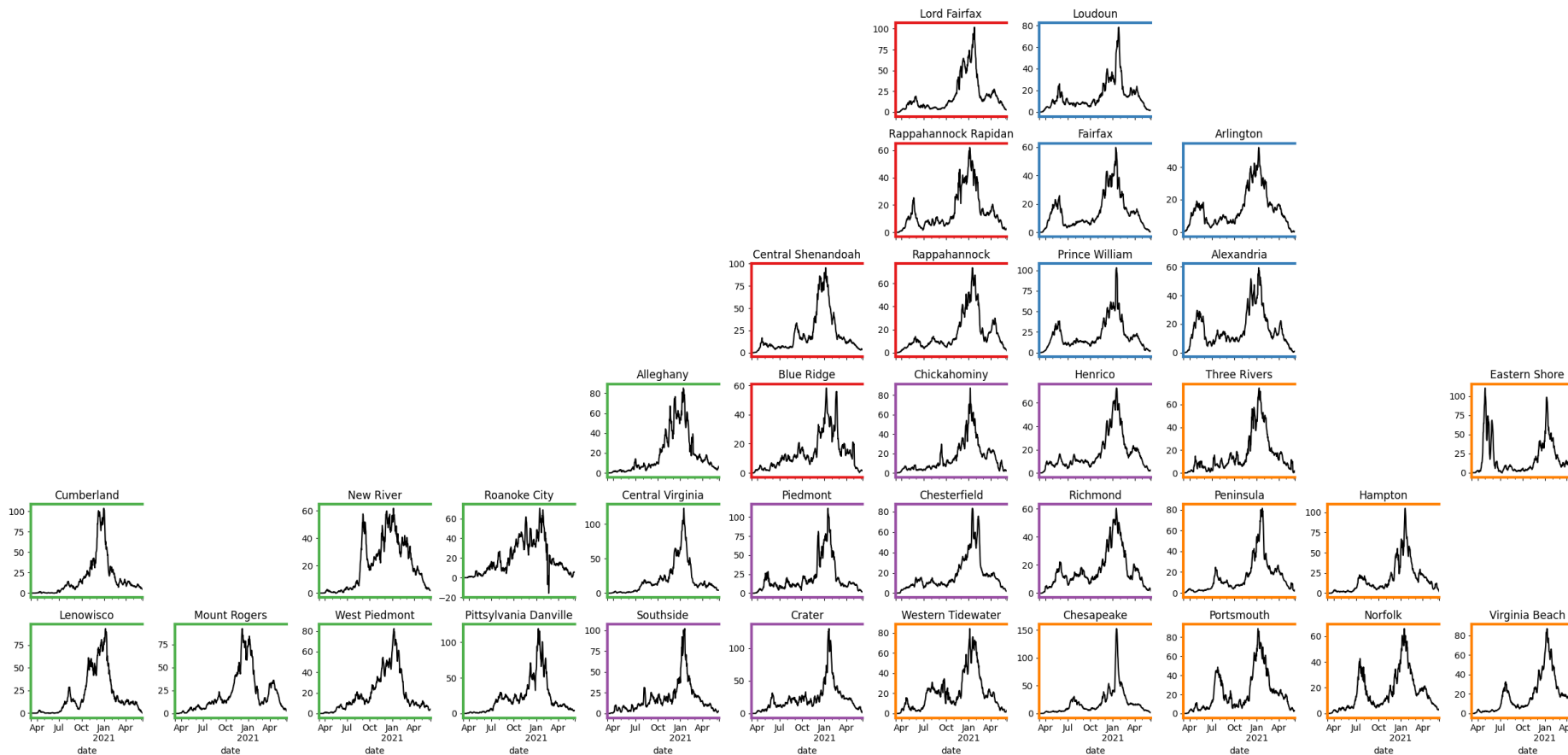
Even without perfect projections, we can confidently draw conclusions:

- **Case rates in Virginia continue to decline though some districts have small rebounds in rates**
- VA mean weekly incidence down to 2.3/100K from 4/100K, US flattening remaining at 5/100K
- Vaccination rates continue to decline after rebound from 12-16 year-olds
- Forecasts show short-term declining rates across Commonwealth
- CDC coordinated ScenarioHub update shows potential impact of novel variants against different levels of vaccine coverage

The situation continues to change. Models continue to be updated regularly.

Situation Assessment

Case Rates (per 100k) and Test Positivity



<https://data.cms.gov/stories/s/q5r5-gjyu>

County level test positivity from RT-PCR tests.

Green: <5.0%
(or with <20 tests in past 14 days)

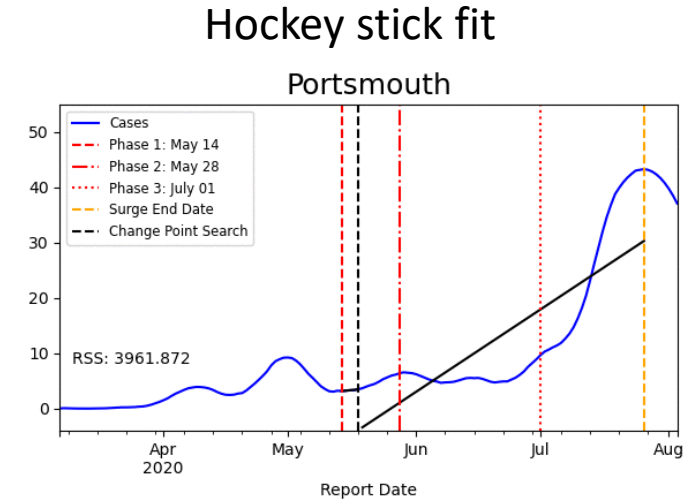
Yellow: 5.0%-10.0%
(or with <500 tests and <2000 tests/100k and >10% positivity over 14 days)

Red: >10.0%
(and not "Green" or "Yellow")

District Trajectories

Goal: Define epochs of a Health District's COVID-19 incidence to characterize the current trajectory

Method: Find recent peak and use hockey stick fit to find inflection point afterwards, then use this period's slope to define the trajectory

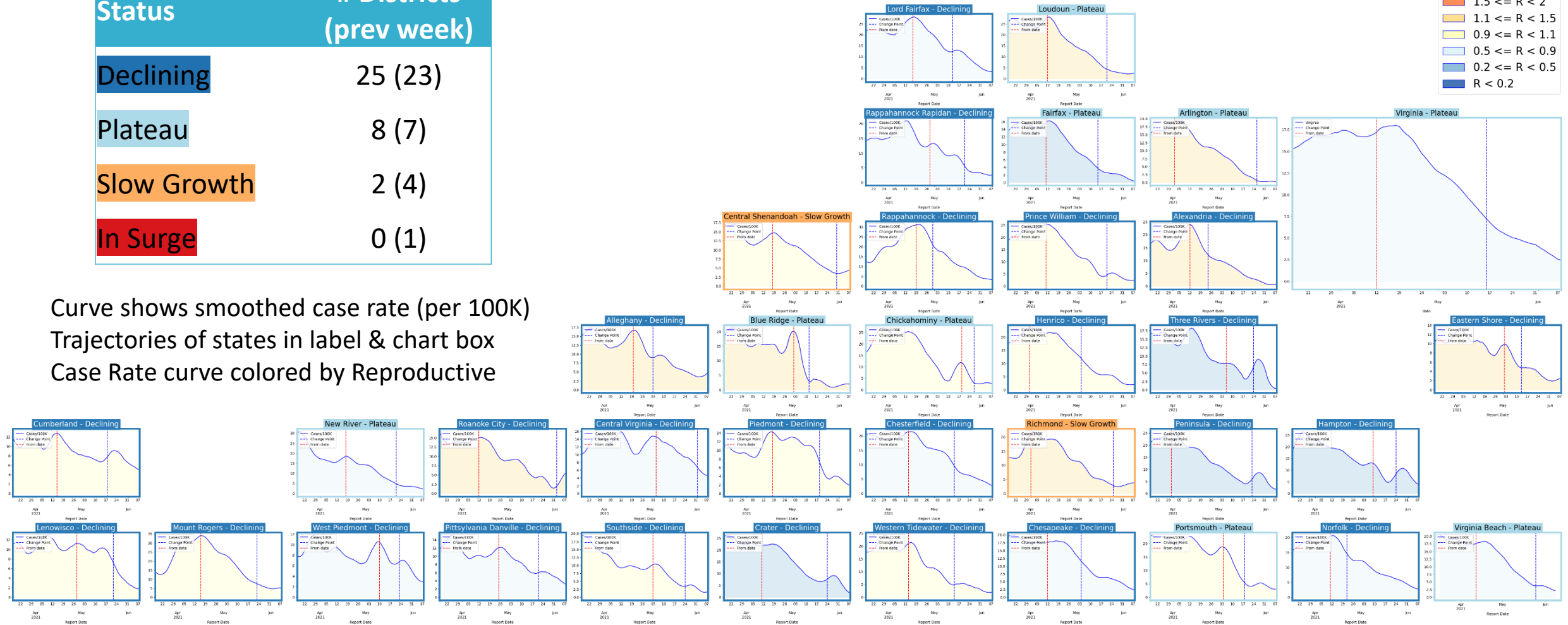


Trajectory	Description	Weekly Case Rate (per 100K) bounds	# Districts (prev week)
Declining	Sustained decreases following a recent peak	below -0.9	25 (23)
Plateau	Steady level with minimal trend up or down	above -0.9 and below 0.5	8 (7)
Slow Growth	Sustained growth not rapid enough to be considered a Surge	above 0.5 and below 2.5	2 (4)
In Surge	Currently experiencing sustained rapid and significant growth	2.5 or greater	0 (1)

District Trajectories – last 10 weeks

Status	# Districts (prev week)
Declining	25 (23)
Plateau	8 (7)
Slow Growth	2 (4)
In Surge	0 (1)

Curve shows smoothed case rate (per 100K)
Trajectories of states in label & chart box
Case Rate curve colored by Reproductive



Estimating Daily Reproductive Number

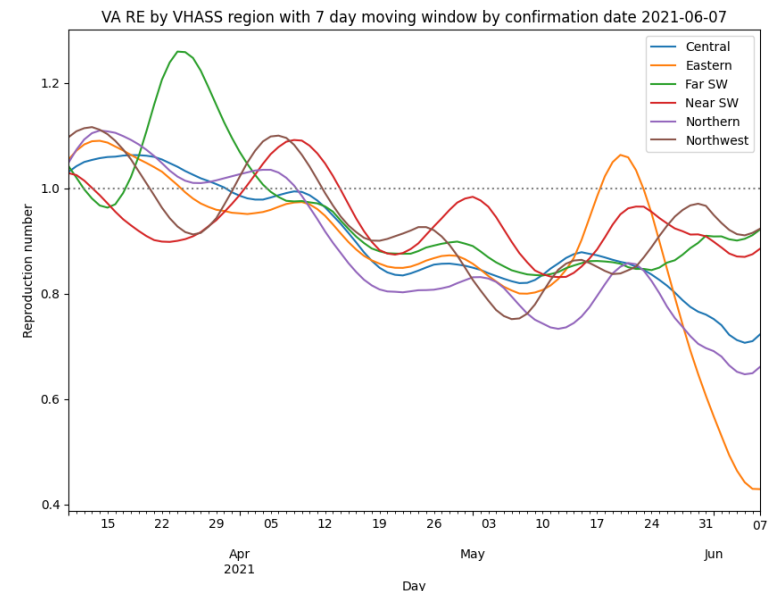
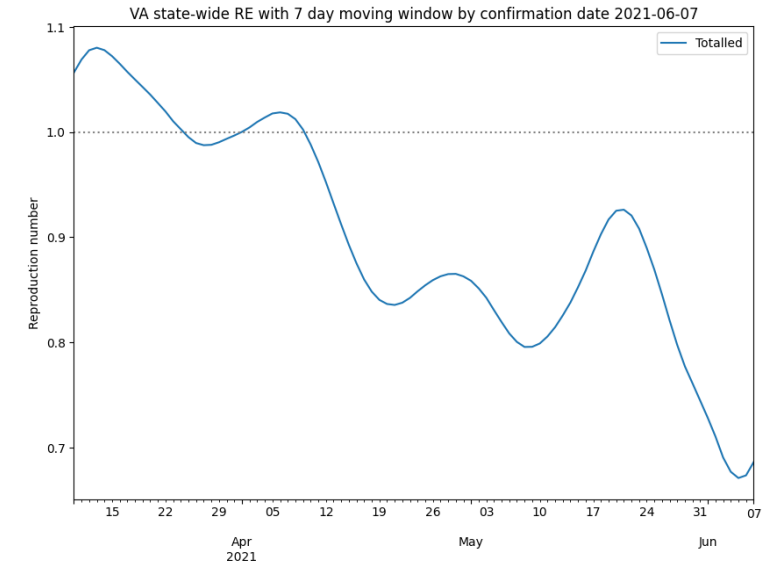
June 7th Estimates

Region	Date Confirmed R_e	Date Confirmed Diff Last Week
State-wide	0.686	-0.174
Central	0.723	-0.163
Eastern	0.429	-0.511
Far SW	0.922	0.151
Near SW	0.885	-0.022
Northern	0.661	-0.089
Northwest	0.923	0.045

Methodology

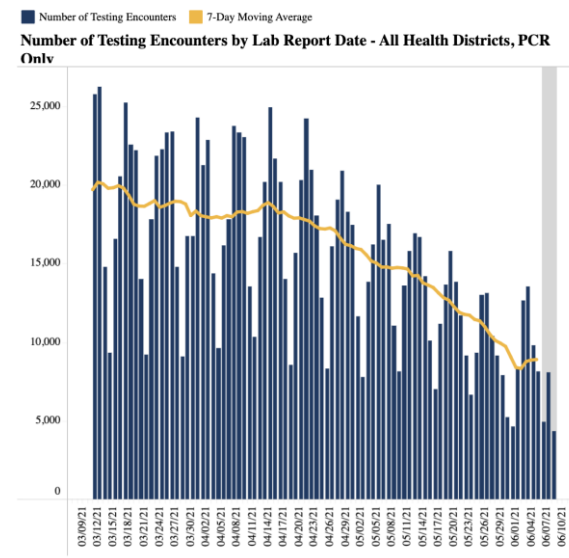
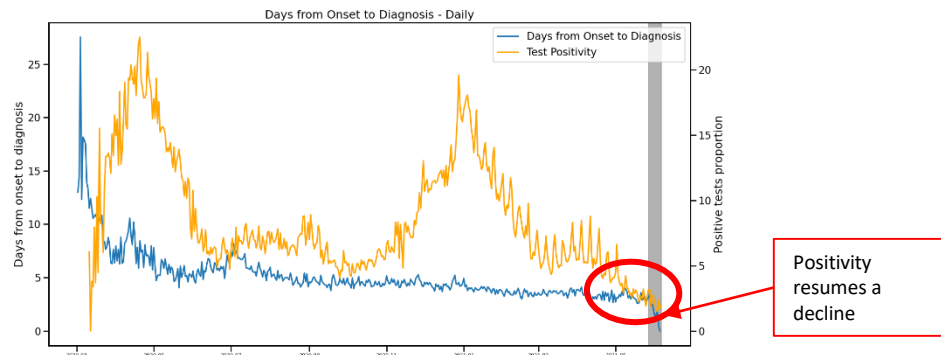
- Wallinga-Teunis method (EpiEstim¹) for cases by confirmation date
- Serial interval: updated to discrete distribution from observations (mean=4.3, Flaxman et al, Nature 2020)
- Using Confirmation date since due to increasingly unstable estimates from onset date due to backfill

1. Anne Cori, Neil M. Ferguson, Christophe Fraser, Simon Cauchemez. A New Framework and Software to Estimate Time-Varying Reproduction Numbers During Epidemics. American Journal of Epidemiology, Volume 178, Issue 9, 1 November 2013, Pages 1505–1512, <https://doi.org/10.1093/aje/kwt133>



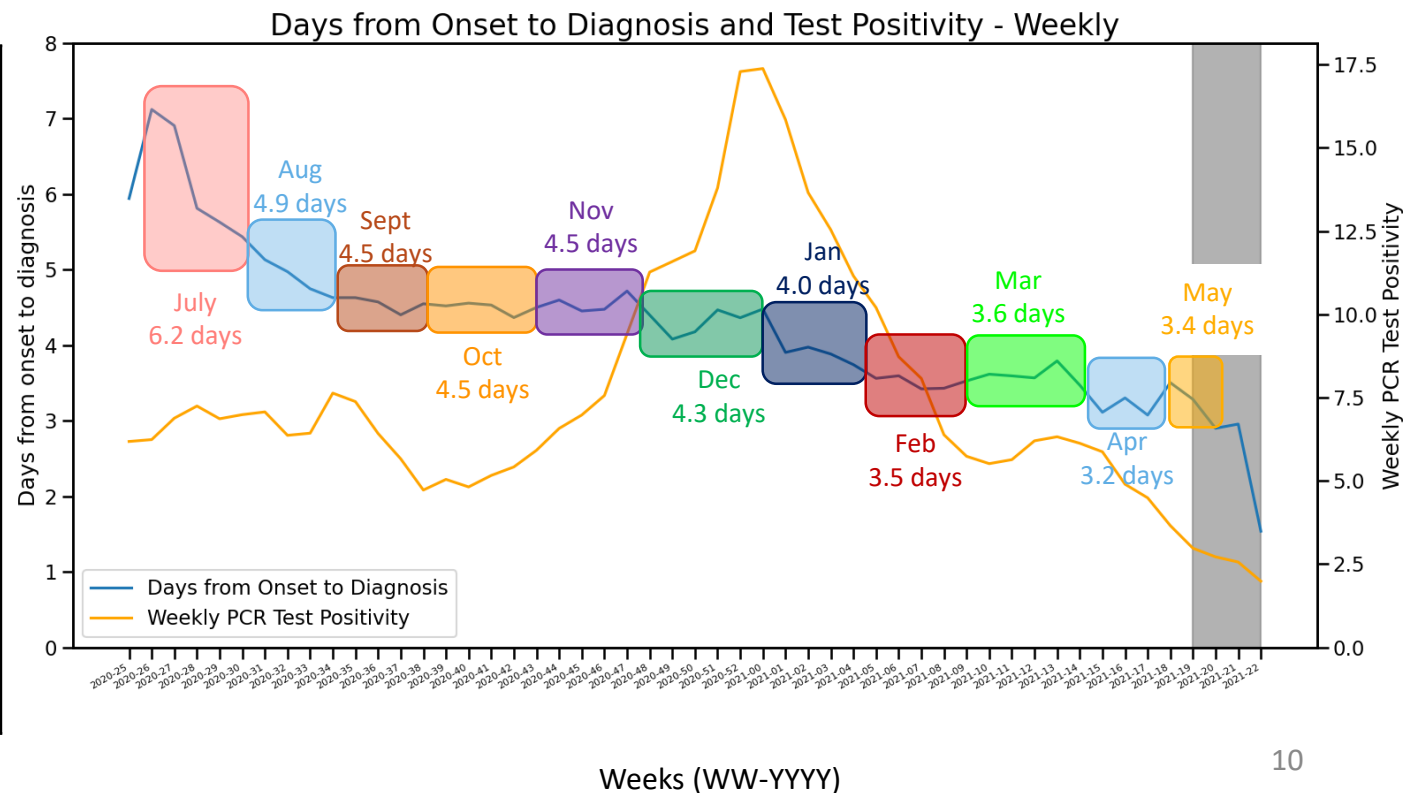
Changes in Case Detection

Test positivity vs. Onset to Diagnosis

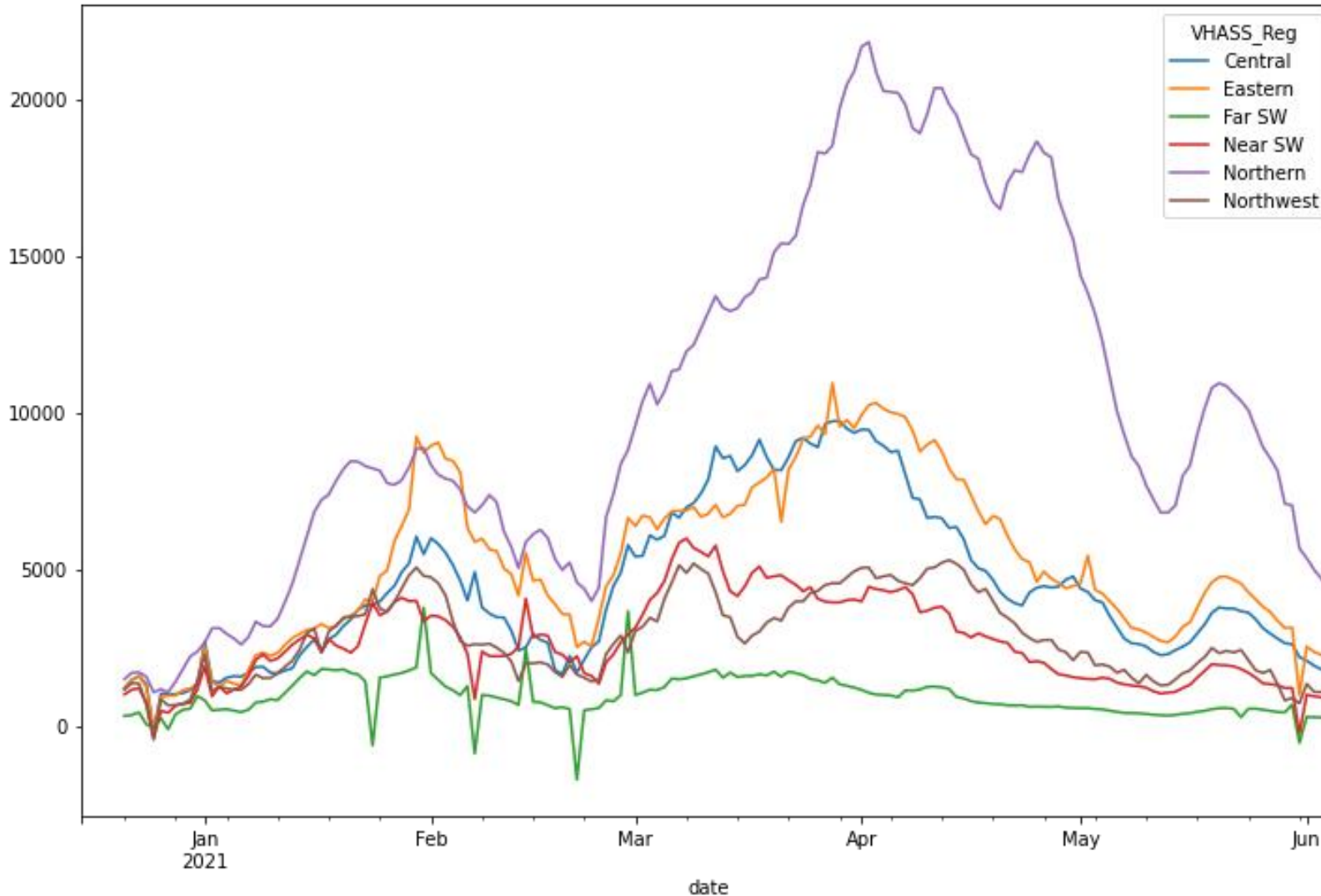


Accessed 9:00am June 9, 2021
<https://www.vdh.virginia.gov/coronavirus/>

Timeframe (weeks)	Mean days	% difference from overall mean
July (26-30)	6.2	-2%
Aug (31-34)	4.9	-22%
Sept (35-38)	4.5	-28%
Oct (39-43)	4.5	-28%
Nov (44-47)	4.5	-27%
Dec (48-49)	4.3	-31%
Jan (00-04)	4.0	-36%
Feb (05-08)	3.5	-44%
Mar (09-13)	3.6	-42%
Apr (14-17)	3.2	-48%
May (18-19)	3.4	-46%
Overall (13 - 19)	6.3	--

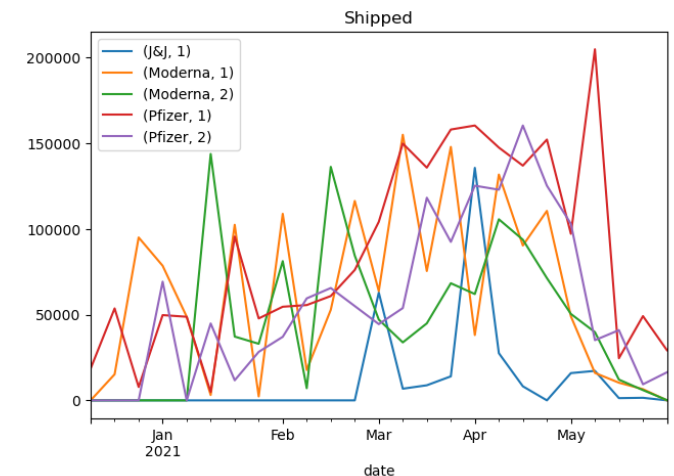


Vaccination Administration Slows



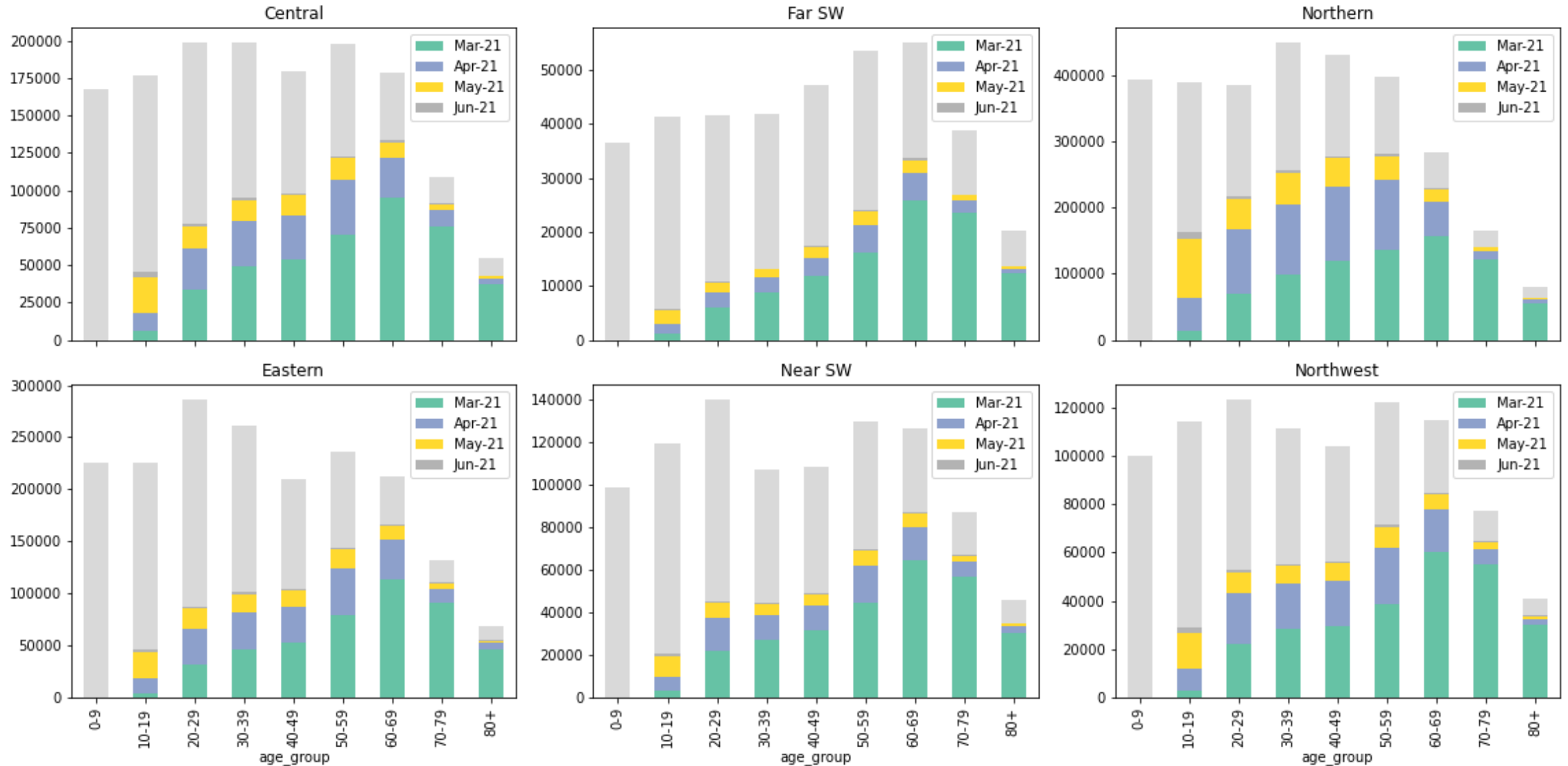
Regional Vaccine courses initiated per day:

- Total counts of first dose of vaccines across regions
- Recent rise due to opening of vaccinations to 12-16 year olds



Shipments have slowed with decreased demand

Vaccinations Shift to Younger Populations

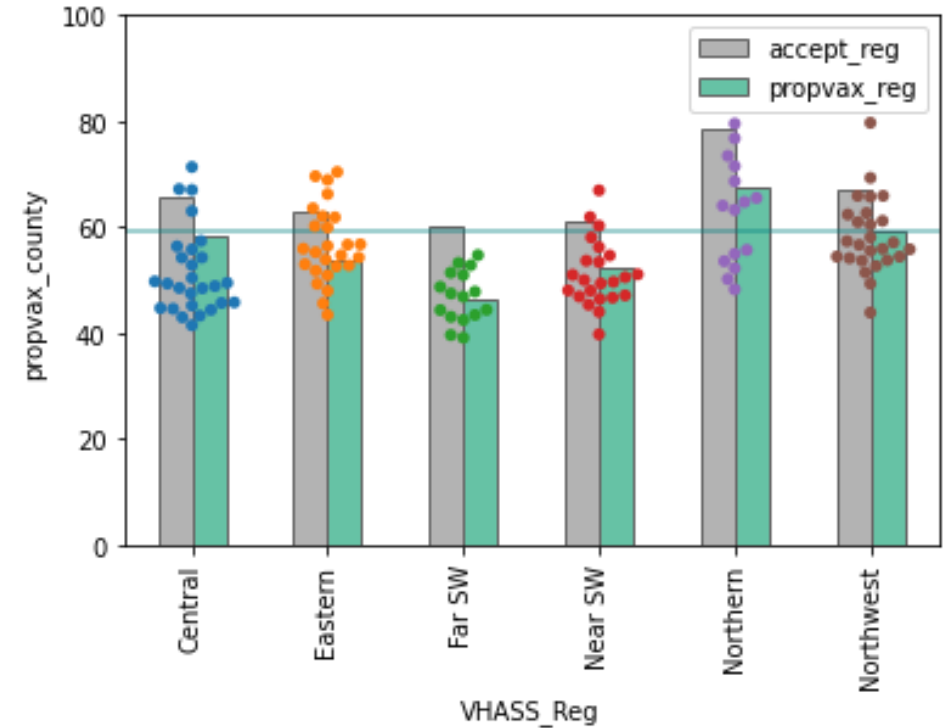


Vaccination Acceptance by Region

Corrections to surveys:

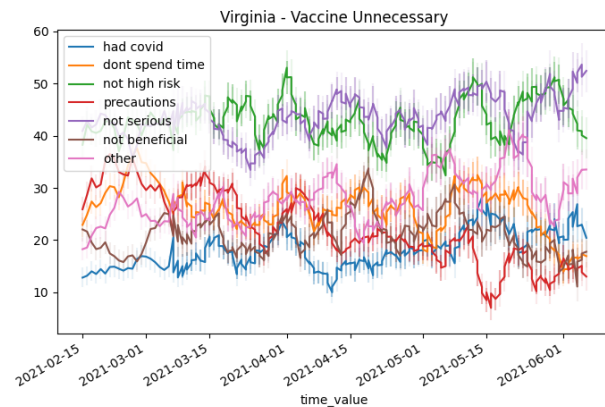
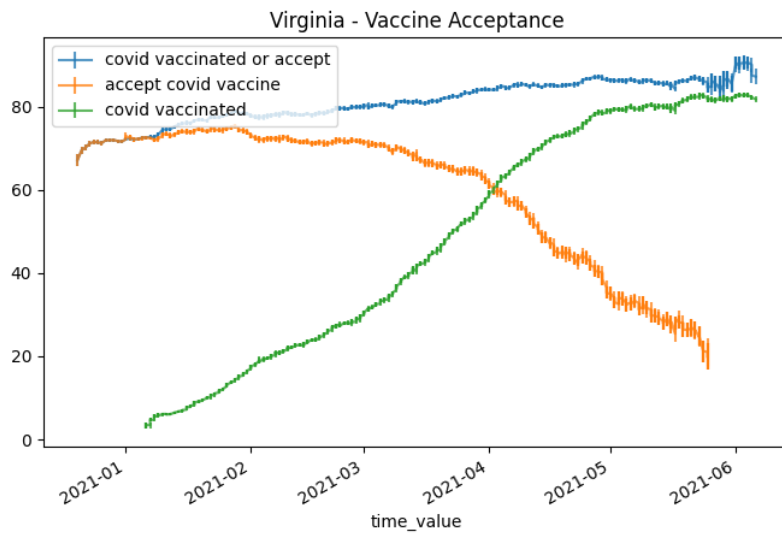
- Facebook administered survey is timely and broad, but biased by who accesses Facebook and answers the survey
- Correction approach:
 - Calculate an over-reporting fraction based on reported vaccinations compared to VDH administration data
 - Cross-validate coarse corrections against HPS survey at the state level and corrected in same manner

Region	COVIDcast accepting corrected	COVIDcast accepting corrected (last week)	VDH proportion vaccinated	COVIDcast reported vaccinated
Central	66%	68%	58%	82%
Eastern	62%	58%	52%	84%
Far SW	60%	53%	41%	66%
Near SW	61%	60%	51%	75%
Northern	78%	80%	67%	88%
Northwest	67%	67%	58%	79%



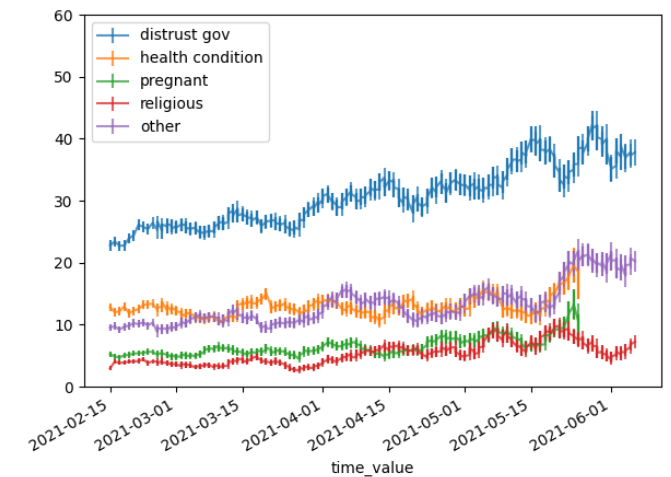
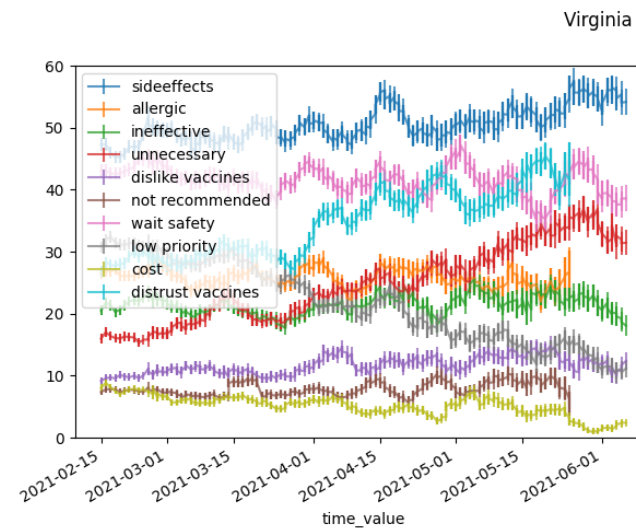
Grey Bar: Survey measured and corrected acceptance
Green Bar: Proportion of eligible population administered a vaccine
Dots: Proportion administered at least one dose for each county

Vaccine Acceptance in Virginia - COVIDcast



Acceptance remains high:

- Proportion of Virginians that have already or would definitely or probably accept vaccination if offered today
- *Survey respondents are reporting high levels of vaccination of ~80% reflecting bias of the mechanism*
- **Top reasons for hesitancy:** side effects, distrust (increasing), unnecessary (increasing)
- **More likely to take if recommended by:** doctors and friends
- **Reasons unnecessary:** Not serious, not high risk, or other



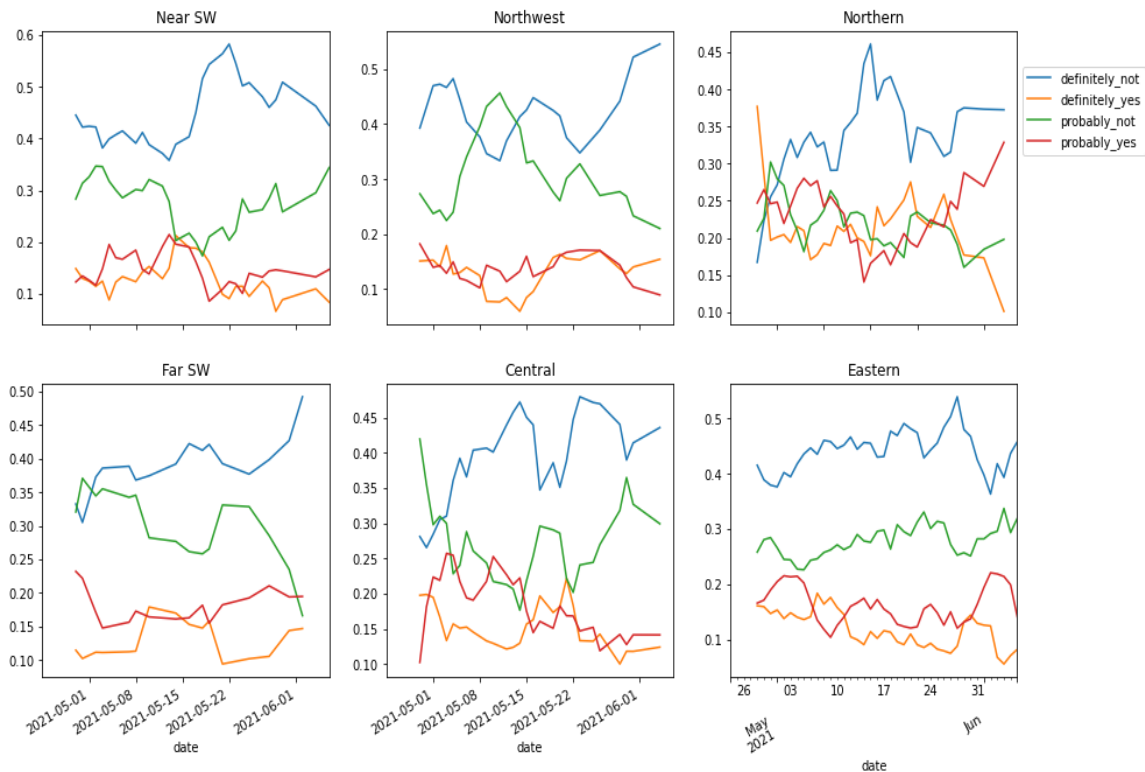
Data Source: <https://covidcast.cmu.edu>

Vaccine Acceptance by Region- COVIDcast

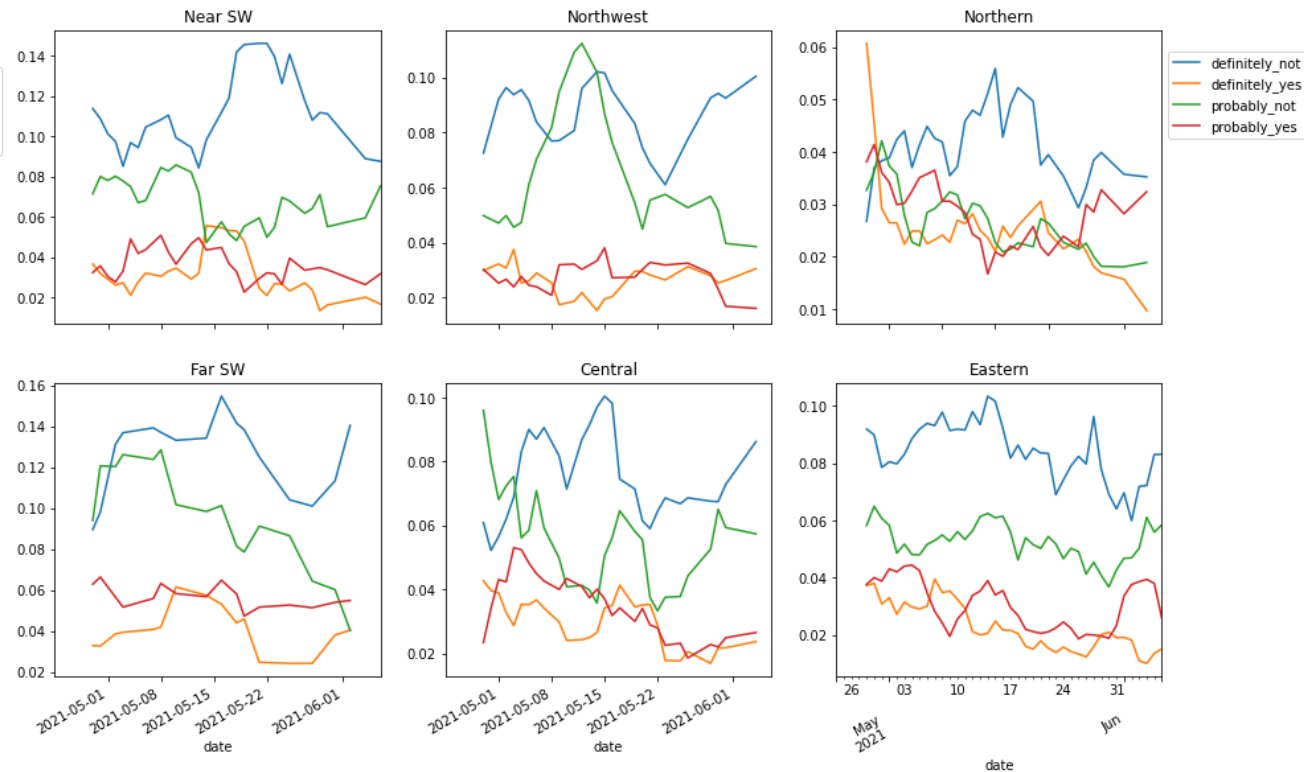
Levels of Acceptance and potential acceptance in flux:

- Nearly all the “Definitely Yes” have been vaccinated, yet there are 5-10% remaining across the regions
- Northwest and Southwest (to lesser degree) see growth in “probably not”, seemingly from “definitely not”

Unvaccinated Only



All Respondents



Data Source: <https://covidcast.cmu.edu>

9-Jun-21

SARS-CoV2 Variants of Concern

Emerging new variants will alter the future trajectories of pandemic and have implications for future control

- Emerging variants can:
 - Increase transmissibility
 - Increase severity (more hospitalizations and/or deaths)
 - Limit immunity provided by prior infection and vaccinations
- Genomic surveillance remains very limited
 - Challenges ability to estimate impact in US to date and estimation of arrival and potential impact in future

	New WHO Name	Transmissibility	Immune Evasiveness	Vaccine Effectiveness [^]
Ancestral		—	—	✓
D614G		+	—	✓
B.1.1.7	Alpha	+++	—	✓
B.1.351	Beta	+	++++	✓
P.1	Gamma	++	++	✓
B.1.429	Epsilon	+	+	✓
B.1.526	Iota	+	+	✓
B.1.617.2	Delta	++++*	++ [#]	✓

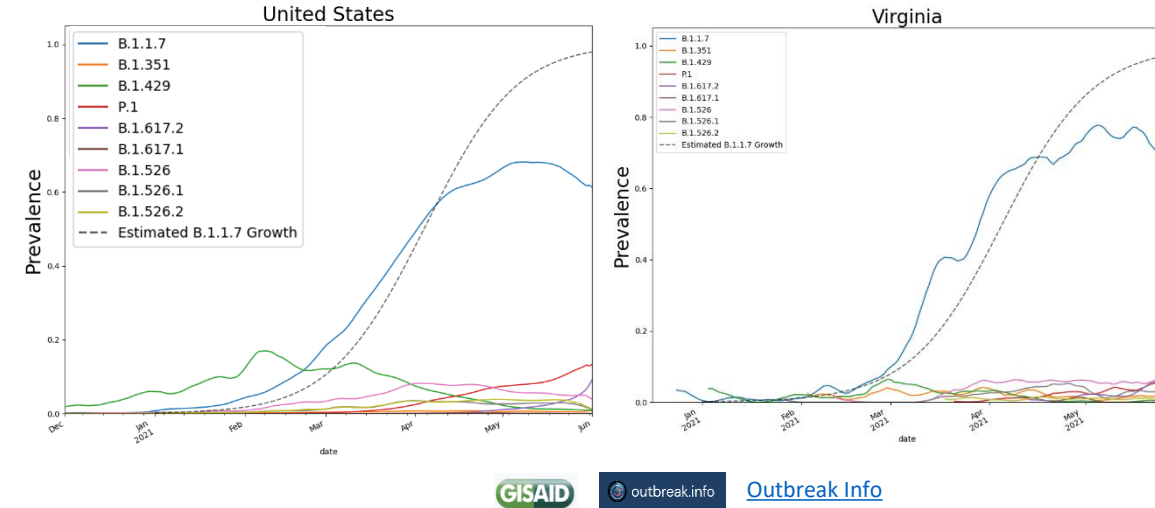
[^]Relative transmissibility to B.1.1.7 yet to be fully defined

^{*}Effectiveness from real world evidence vs. severe illness, not all vaccines are effective vs all variants, and importance of 2-doses, especially for B.1.617.2 for which 1 dose of mRNA or AZ is only ~30% effective [#] May carry more immune escape than P.1, to be determined

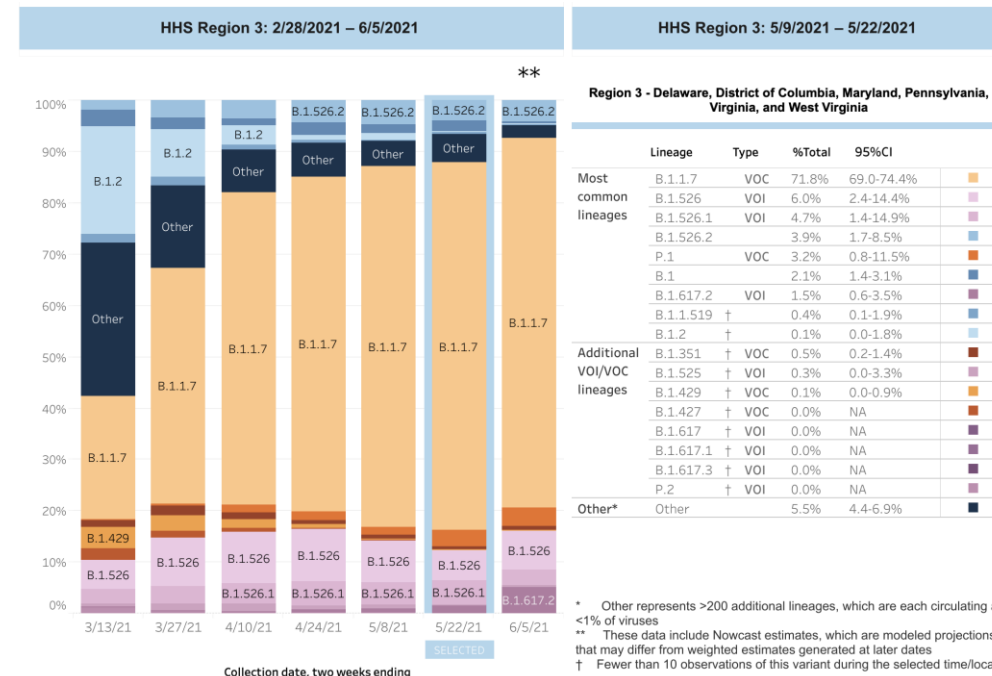


World Health Organization

WHO and Eric Topol



[Outbreak Info](https://www.outbreak.info)



CDC
Variant
Tracking

* Other represents >200 additional lineages, which are each circulating at <1% of viruses
 ** These data include Nowcast estimates, which are modeled projections that may differ from weighted estimates generated at later dates
 † Fewer than 10 observations of this variant during the selected time/loc...

SARS-CoV2 Variants of Concern

Alpha α - Lineage B.1.1.7

Prevalence: Levels have rapidly risen, as anticipated, and now are plateauing at national level and in many states, seemingly in VA as well

Transmissibility: Estimated increase of 50% compared to previous variants. B.1.1.7's mutations aid its infection efficiency, and thus boosts its overall levels of viremia; [study from Public Health England](#) shows contacts of B.1.1.7 cases are more likely (50%) to test positive than contacts of non-B.1.1.7 patients

Severity: Increased viremia also appears to increase the risk of hospitalization (60%) and mortality (60%). [Danish](#) study shows B.1.1.7 to have a 64% higher risk of hospitalization, while [Public Health Scotland](#) studies showed a range of 40% to 60%; [Study in Nature](#) based on UK data estimates B.1.1.7 cases have 60% higher mortality

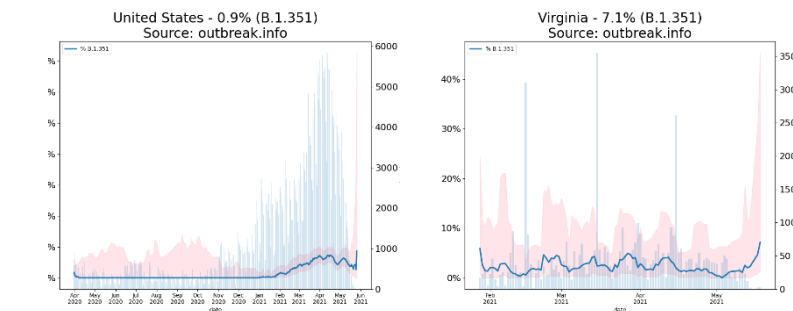
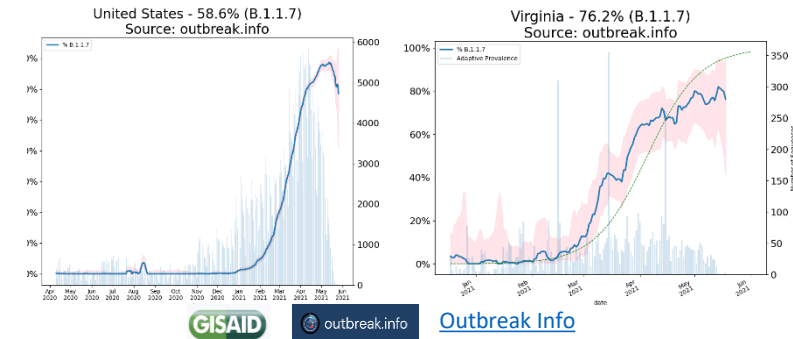
Beta β - Lineage B.1.351

Prevalence: Levels have remained low, as this variant's transmissibility can't compete with B.1.1.7, however, as more of the population becomes immune it may gain an advantage

Immune Escape: Many studies show that convalescent sera from previously infected individuals does not neutralize B.1.351 virus well which is [predictive](#) of [protection](#), however, [vaccine induced immunity](#) shows [signs](#) of [effectiveness](#)

Lineage [B.1.429/427](#) and [B.1.526](#) and subvariants

- Combined account for around 20% of circulating virus, share may be shrinking as B.1.1.7 outcompetes



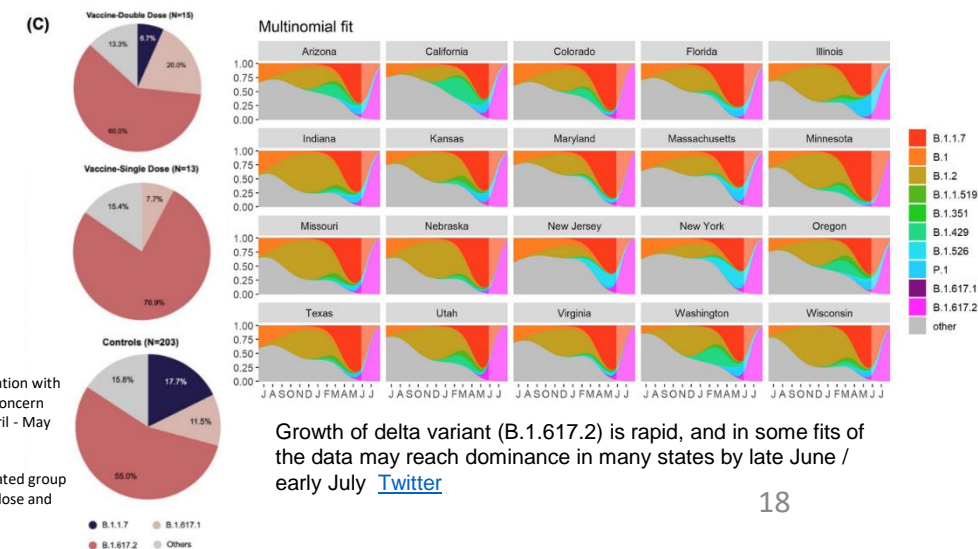
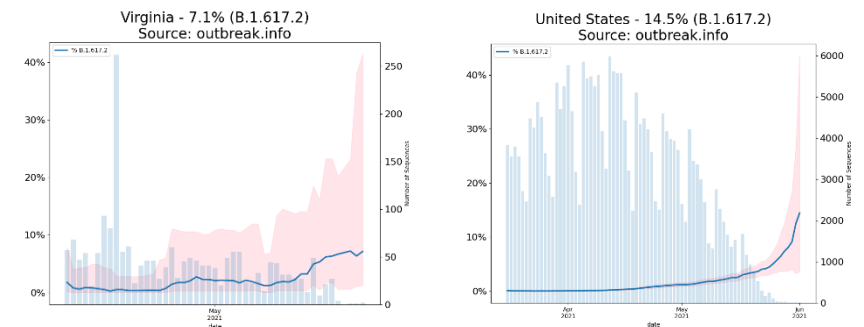
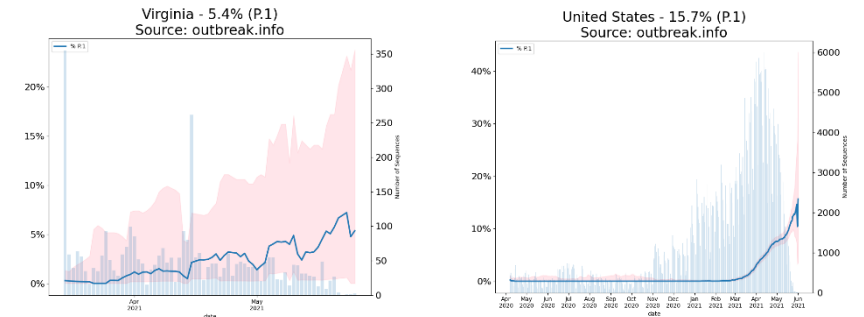
SARS-CoV2 Variants of Concern

Gamma γ - Lineage P.1

- **Prevalence:** Nationally at 15.7%, lower in VA at 5.4%
- New study estimates 17-32% of all infections in Manaus in 2021 were reinfections, which helps explain data from Brazil demonstrating P.1's continued dominance in Rio despite presence of B.1.1.7

Delta δ - Lineage B.1.617.2 and related subvariants

- Continues to drive outbreak in India and neighbors, with continued growth in UK, Europe and in accelerating growth in the US
- Categorized as VoC by Public Health England, WHO, expect CDC to follow
- Several studies estimate B.1.617.2 to be 30-60% more transmissible than B.1.1.7, and also more severe
- More studies show limited immune escape similar to B.1.351, however, still suggest protection remains for vaccinated, though PHE study shows limited efficacy of Astra-Zeneca with only one dose
- A recent study shows that more vaccine breakthrough infections are caused by variants Delta and Alpha

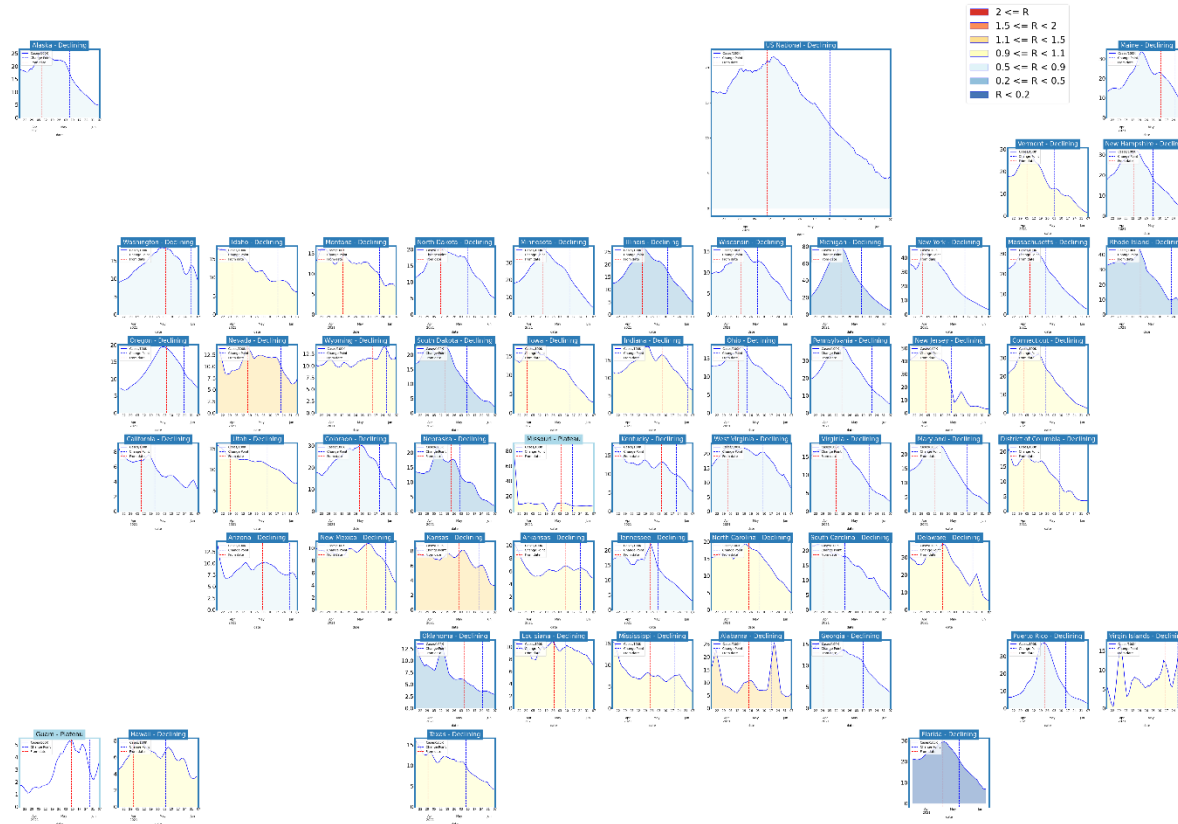


This study elaborates genomic analysis of isolates from symptomatic breakthrough infections following vaccination with AZD1222/Covishield and BBV152/Covaxin. Variants of concern B.1.617.2 and B.1.1.7 responsible for cases surge in April - May 2021 in Delhi, were the predominant lineages among breakthrough infections.

"Suggests B.1.617.2 relative to non-B.1.617.2 in vaccinated group compared to controls is 2.7 (95% CI: 0.7-10) after one dose and 1.2 (0.4-3.6) after two" <https://osf.io/fgd4x/> <https://t.co/lxMifGdVBn>

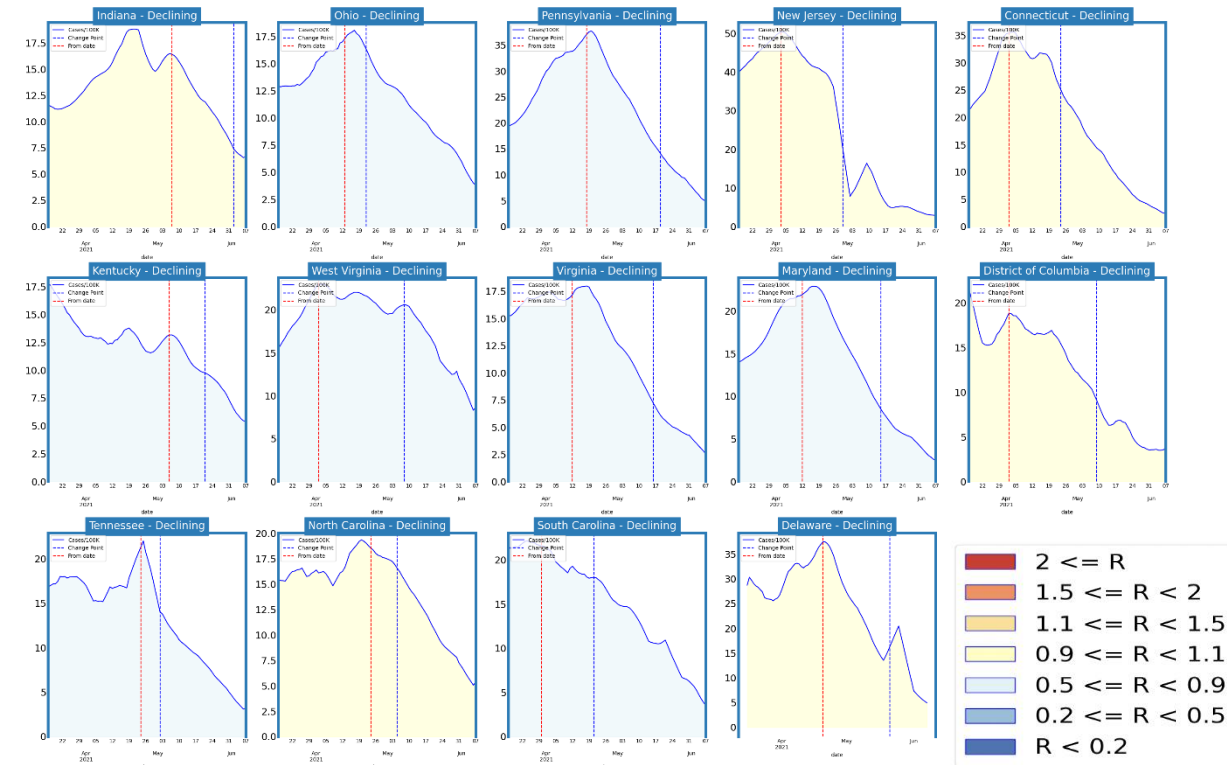
Other State Comparisons

Trajectories of States



- Nearly all states are declining
- Growth out west has slowed, recent reporting artifacts in some states perturb the otherwise calm picture

Virginia and her neighbors

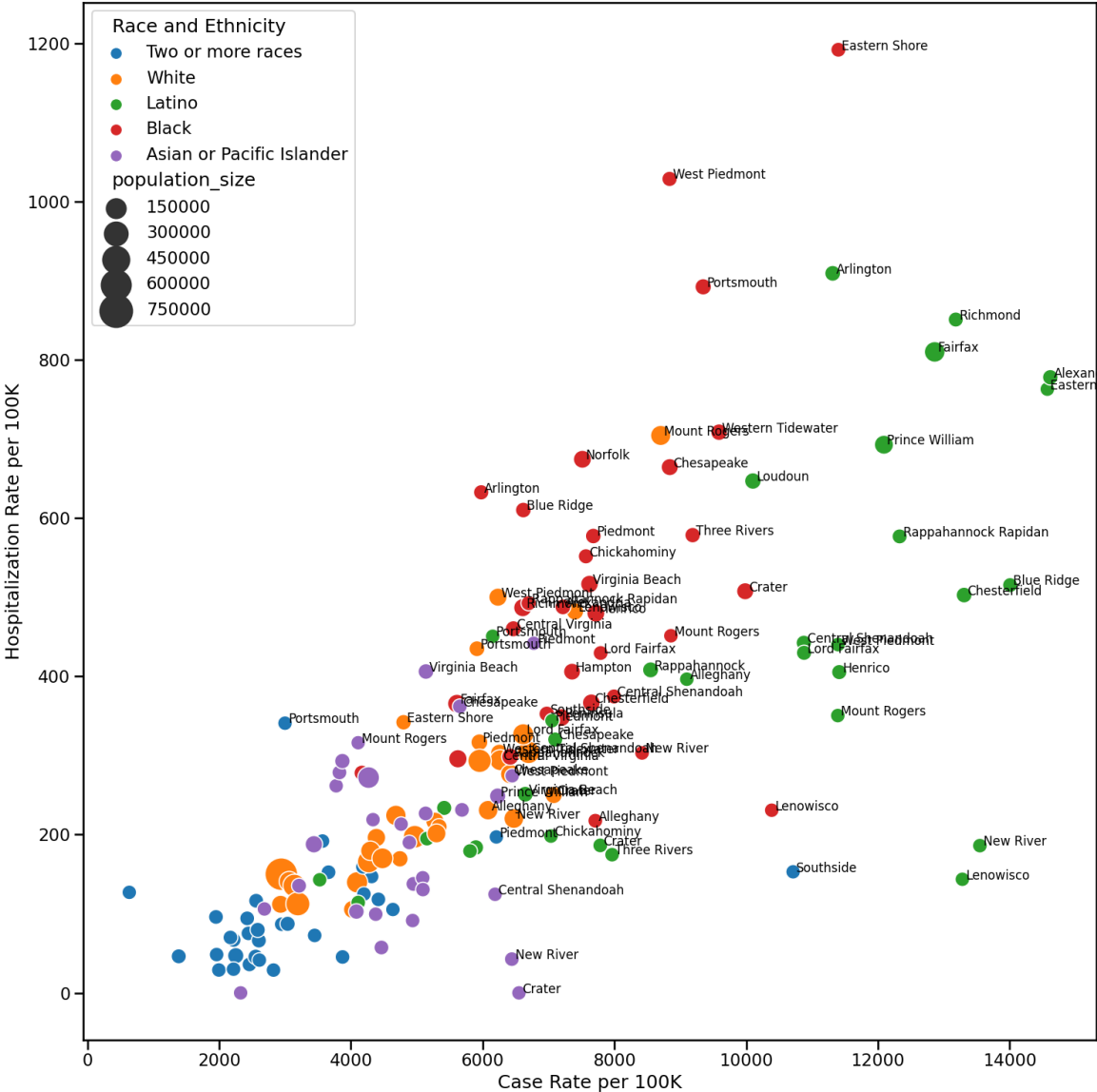


- VA and neighbors are all declining with steady pace
- Most neighbors are now below 10/100K level

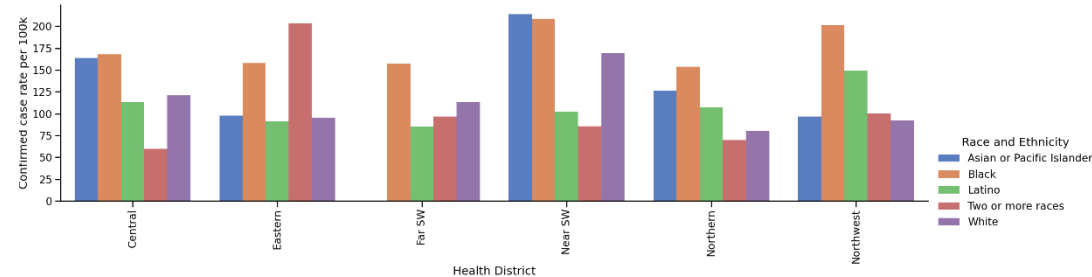
Race and Ethnicity cases per 100K

Rates per 100K of each Racial-Ethnic population by Health District

- Each Health District's Racial-Ethnic population is plotted by their Hospitalization and Case Rate
- Points are sized based on their overall population size (overlapping labels removed)
- Change in rates over the last 2 weeks



Case Rate Change in last 14 days

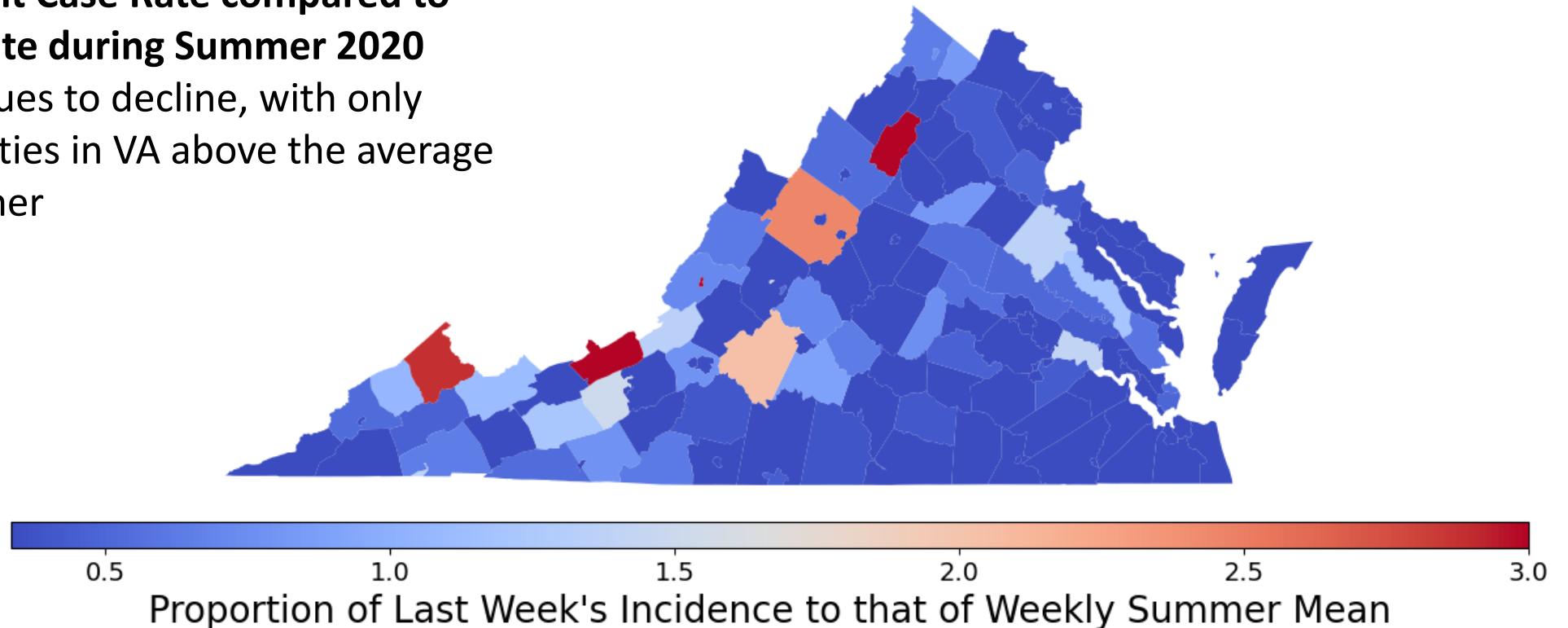


Recent Incidence Compared to Summer 2020

Recent Incidence Compared to Weekly Summer Mean by County
Mean: 0.49; Median: 0.25; IQR: 0.13-0.54

Ratio of Recent Case Rate compared to mean Case Rate during Summer 2020

- Ratio continues to decline, with only 12% of counties in VA above the average of last summer



Zip code level weekly Case Rate (per 100K)

Case Rates in the last week by zip code

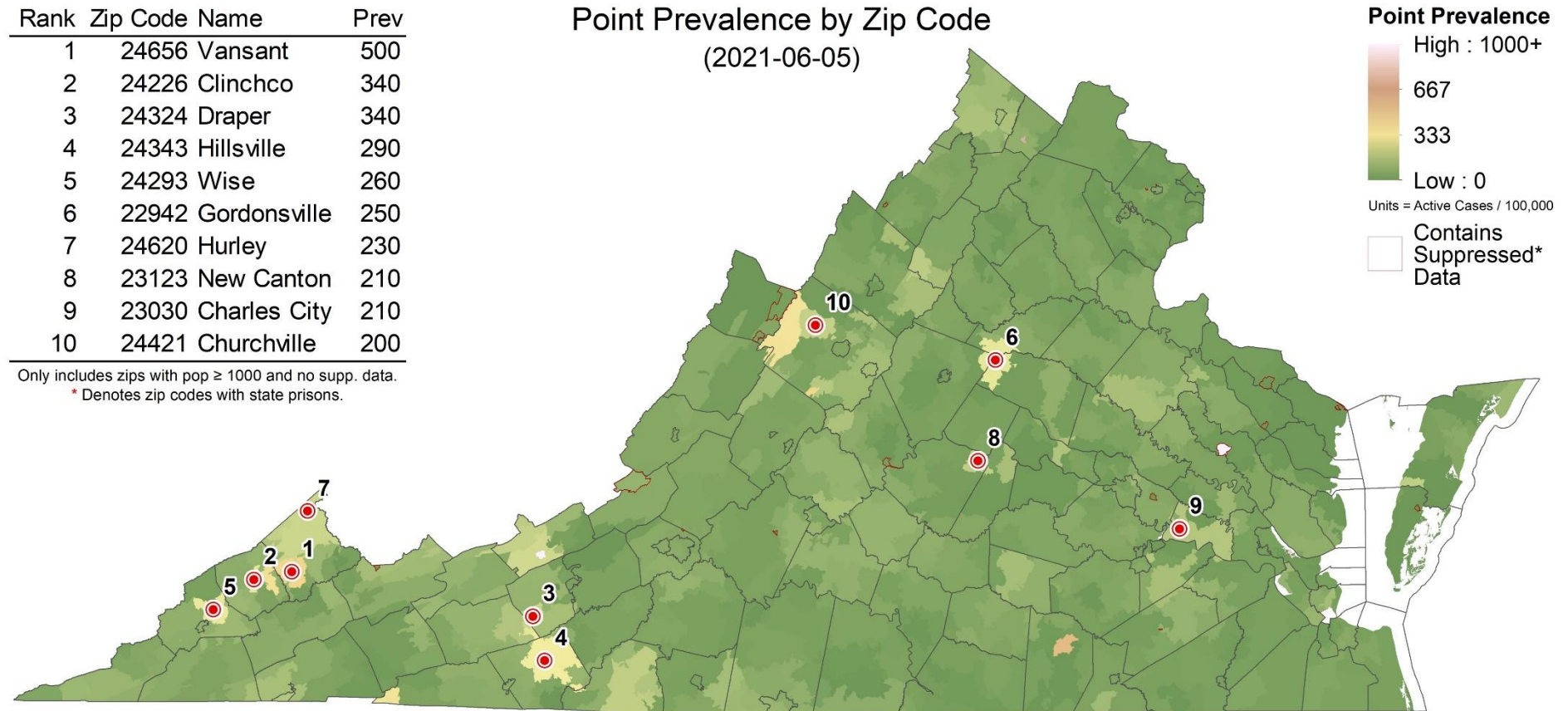
- Adjusted Color gradient to lower rates, thus red is a lower prevalence
- Some counts are low and suppressed to protect anonymity, those are shown in white

Rank	Zip Code	Name	Prev
1	24656	Vansant	500
2	24226	Clinchco	340
3	24324	Draper	340
4	24343	Hillsville	290
5	24293	Wise	260
6	22942	Gordonsville	250
7	24620	Hurley	230
8	23123	New Canton	210
9	23030	Charles City	210
10	24421	Churchville	200

Only includes zips with pop ≥ 1000 and no supp. data.

* Denotes zip codes with state prisons.

Point Prevalence by Zip Code
(2021-06-05)



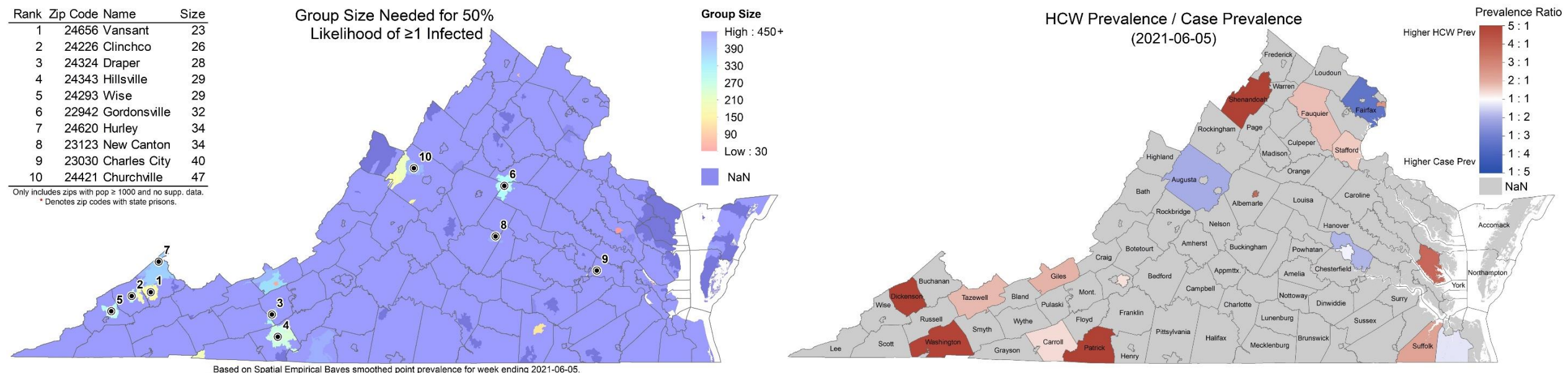
Based on Spatial Empirical Bayes smoothed point prevalence for week ending 2021-06-05.

Note new color ramp since 2021-05-22.

Risk of Exposure by Group Size and HCW prevalence

Case Prevalence in the last week by zip code used to calculate risk of encountering someone infected in a gathering of randomly selected people (group size 25)

- **Group Size:** Assumes 2 undetected infections per confirmed case (ascertainment rate from recent seroprevalence survey), and shows minimum size of a group with a 50% chance an individual is infected by zip code (eg in a group of 23 in Vansant, there is a 50% chance someone will be infected)
- **HCW prevalence:** Case rate among health care workers (HCW) in the last week using patient facing health care workers as the denominator

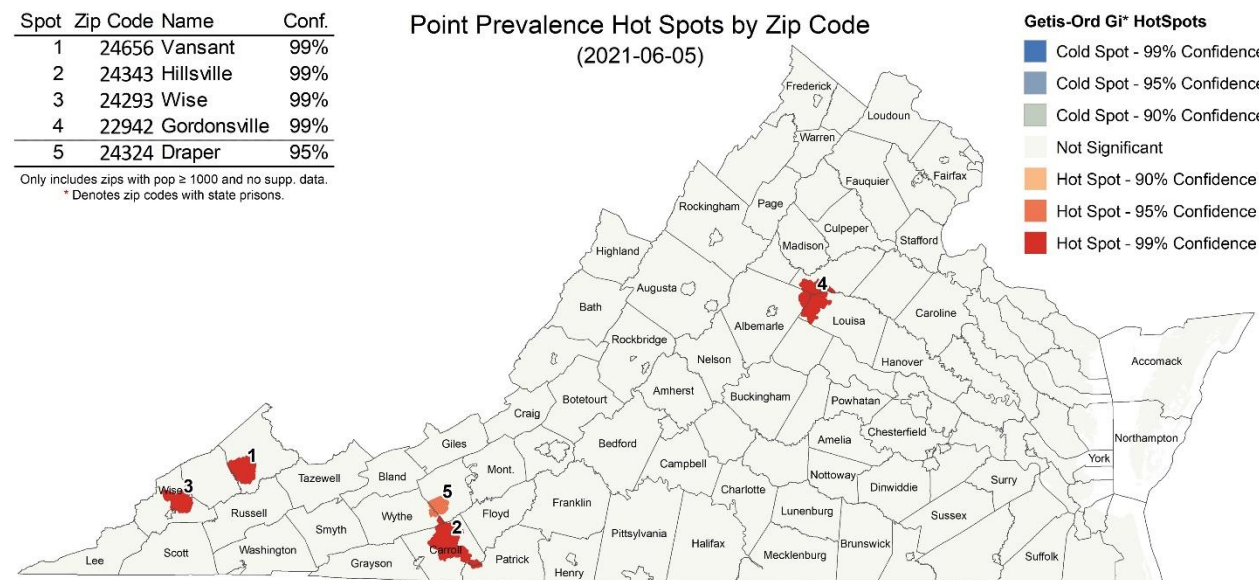


Current Hot-Spots

Case rates that are significantly different from neighboring areas or model projections

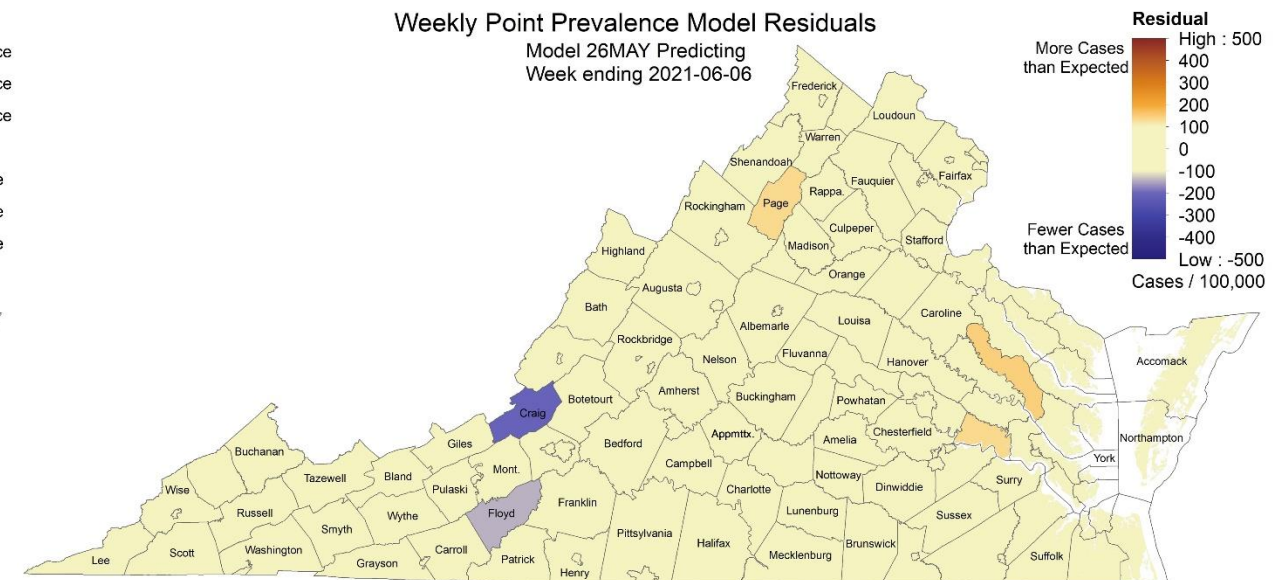
- **Spatial:** SaTScan based hot spots compare clusters of zip codes with weekly case prevalence higher than nearby zip codes to identify larger areas with statistically significant deviations
- **Temporal:** The weekly case rate (per 100K) projected last week compared to observed by county, which highlights temporal fluctuations that differ from the model's projections

Spatial Hotspots



Based on Global Empirical Bayes smoothed point prevalence for week ending 2021-06-05.

Clustered Temporal Hotspots

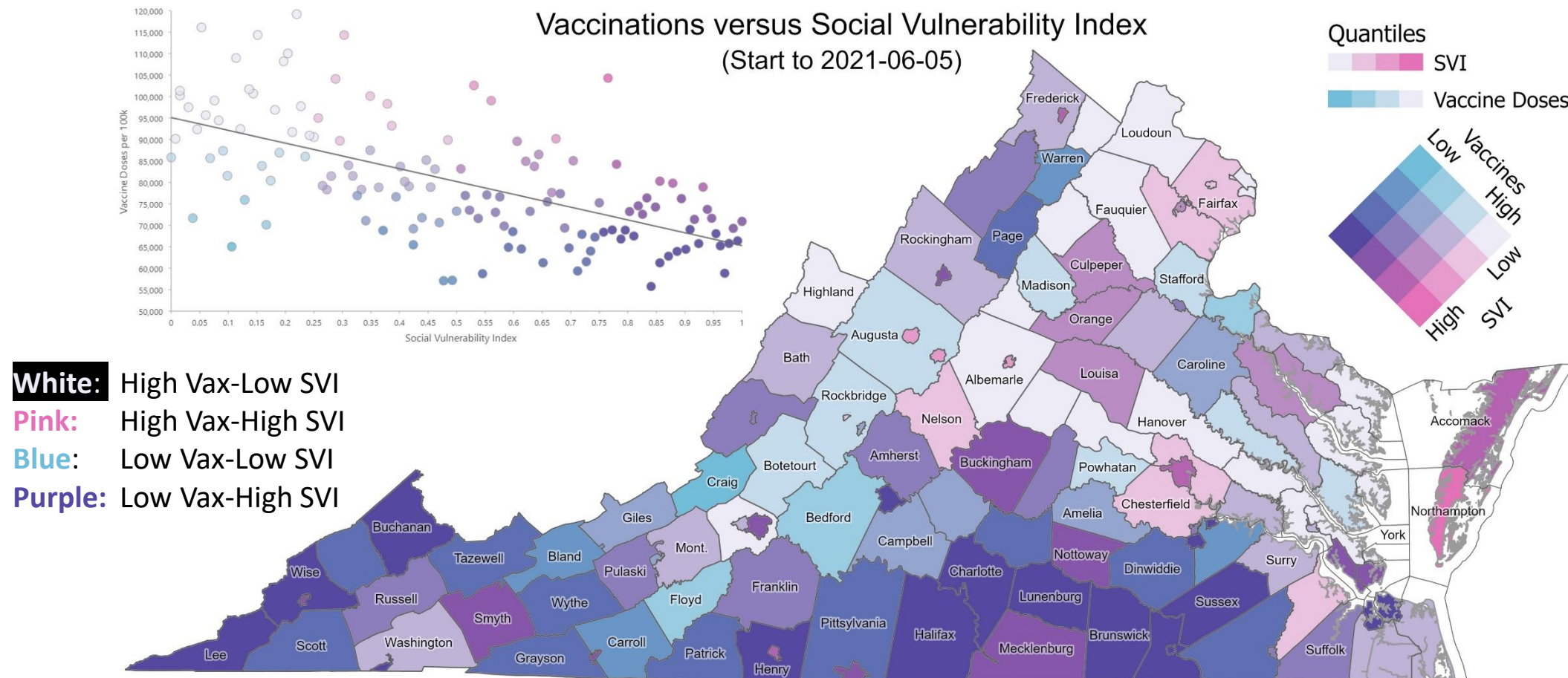


Moran's I = -0.160312, Z-Score = -1.959159, P-Value = 0.050094
Slight Negative Residual Autocorrelation Suspected

Social Vulnerability and Total Vaccination Rates

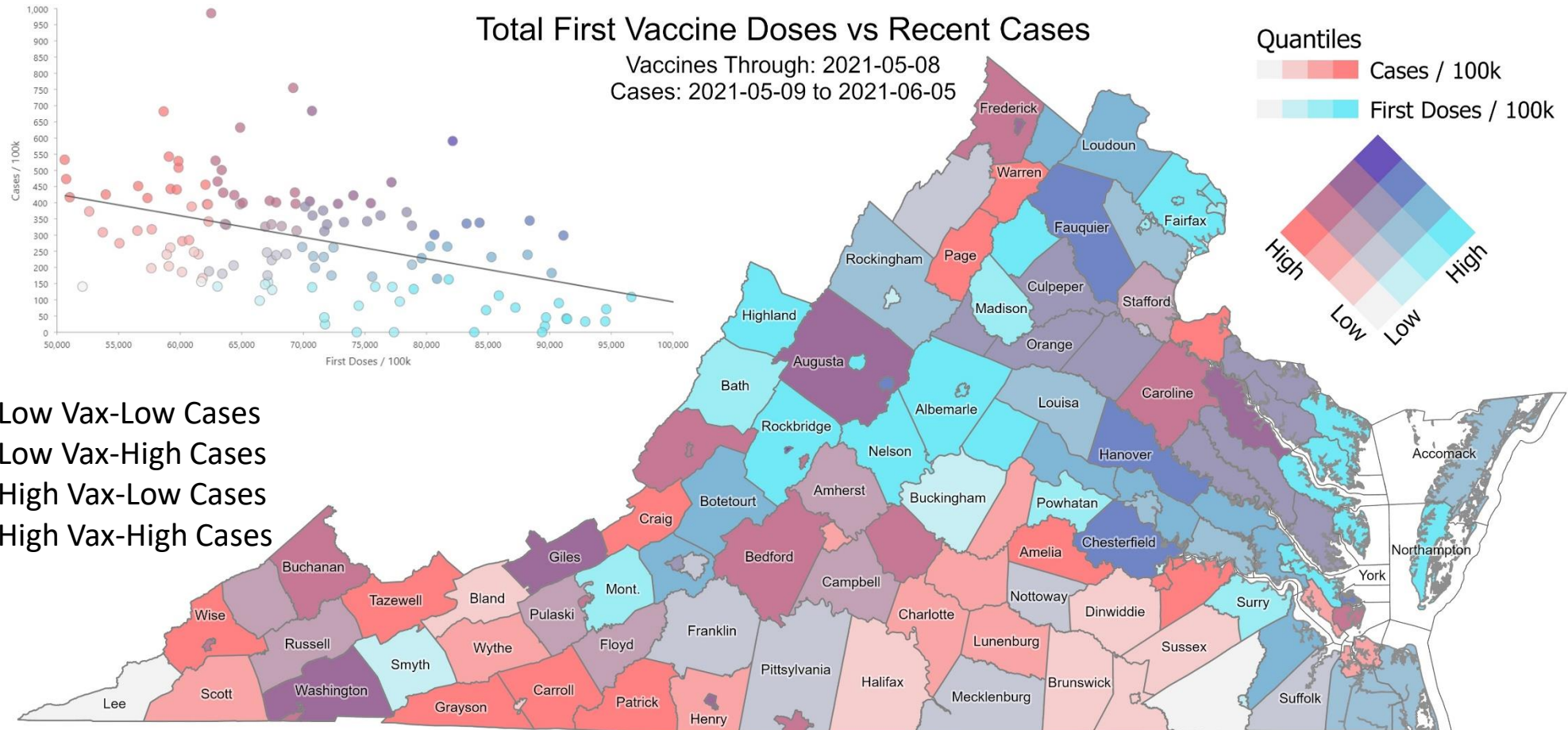
Comparison of social vulnerability and total vaccination rate since the start of vaccination

- **Social Vulnerability:** Each county's Social Vulnerability Index (CDC) compared with the level of vaccination



Vaccination and Recent Case Rates

Comparison of total vaccination rate and case prevalence in the last month



Forecasts and Other Scenarios

Using Ensemble Model to Guide Projections

Ensemble methodology that combines the Adaptive with machine learning and statistical models such as:

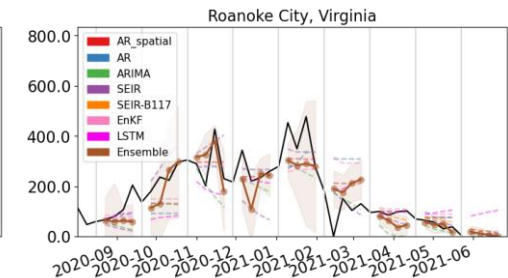
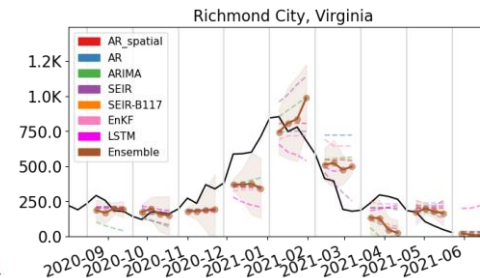
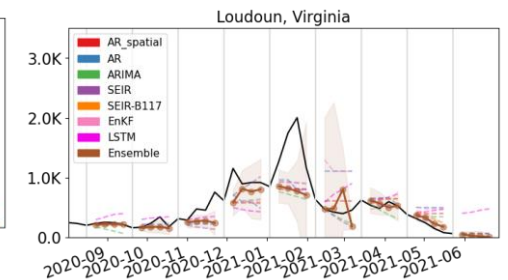
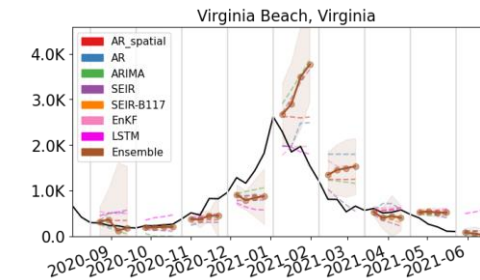
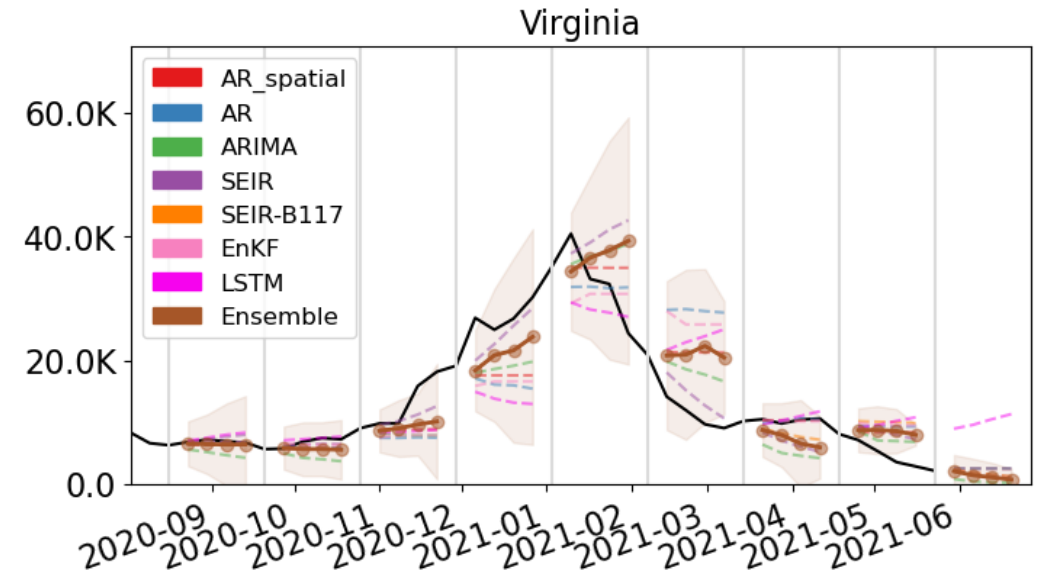
- Autoregressive (AR, ARIMA)
- Neural networks (LSTM)
- Kalman filtering (EnKF)

Weekly forecasts done at county level.

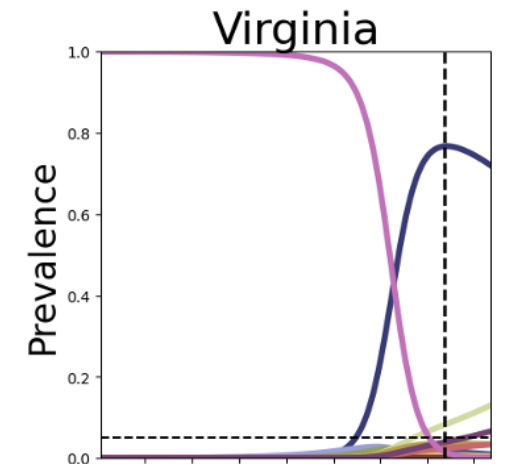
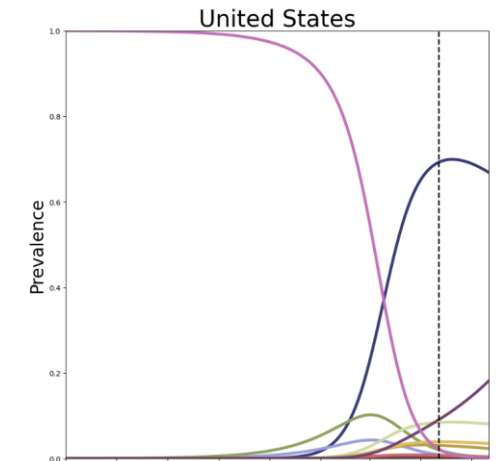
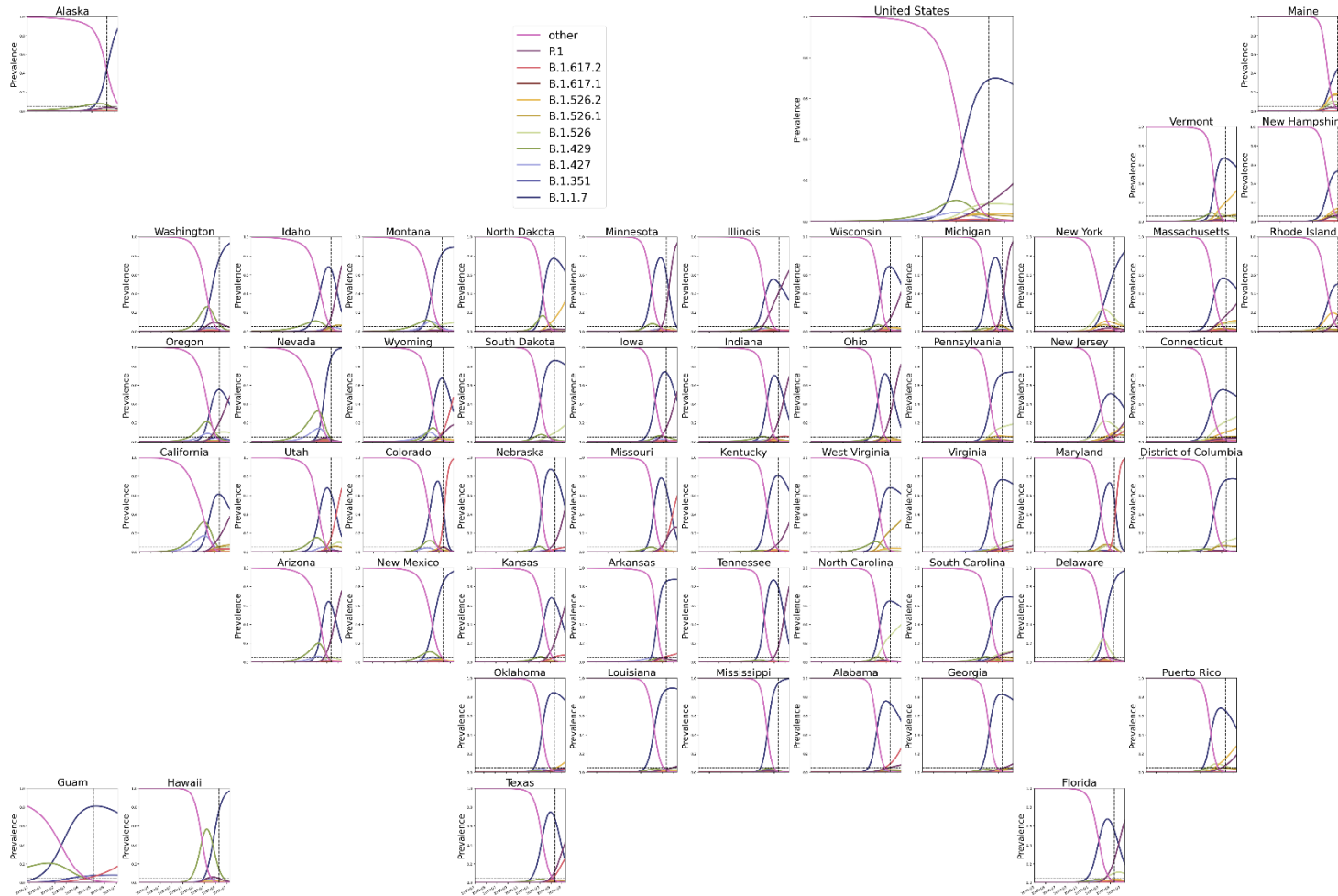
Models chosen because of their track record in disease forecasting and to increase diversity and robustness.

Ensemble forecast provides additional 'surveillance' for making scenario-based projections.

Also submitted to CDC Forecast Hub.



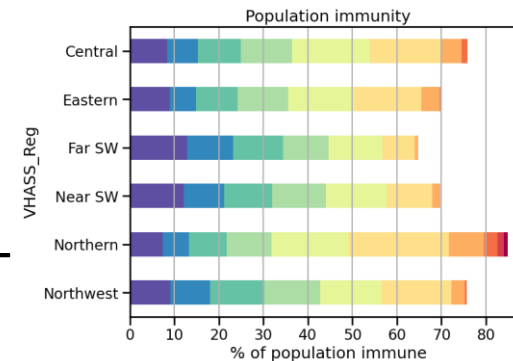
Predicted Variant Prevalence



Virginia's Progress on Population Immunity

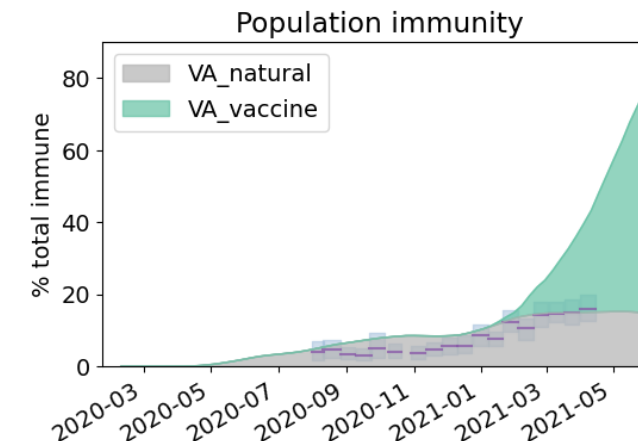
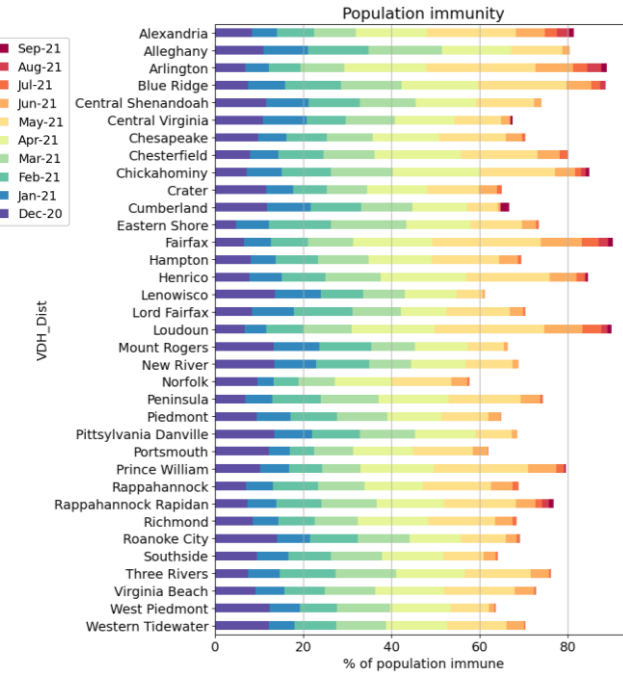
Natural Immunity and Vaccines combine to produce a population level of immunity

- Duration of immunity from infection with SARS-CoV2 still not well understood
 - We assume a conservative 6 month period of protection for these calculations
 - Natural immunity is well calibrated to recent seroprevalence surveys
- Vaccine induced immunity is likely to last longer, we assume indefinite protection
 - This also assumes that all administered vaccines remain protective against current and future novel variants
- Population immunity depends on a very high proportion of the population getting vaccinated
 - Using regional vaccine acceptance



Region	% immune (est.)*
Central	72%
Eastern	68%
Far SW	65%
Near SW	69%
Northern	75%
Northwest	74%
Virginia	72%

* As of June 6, 2021



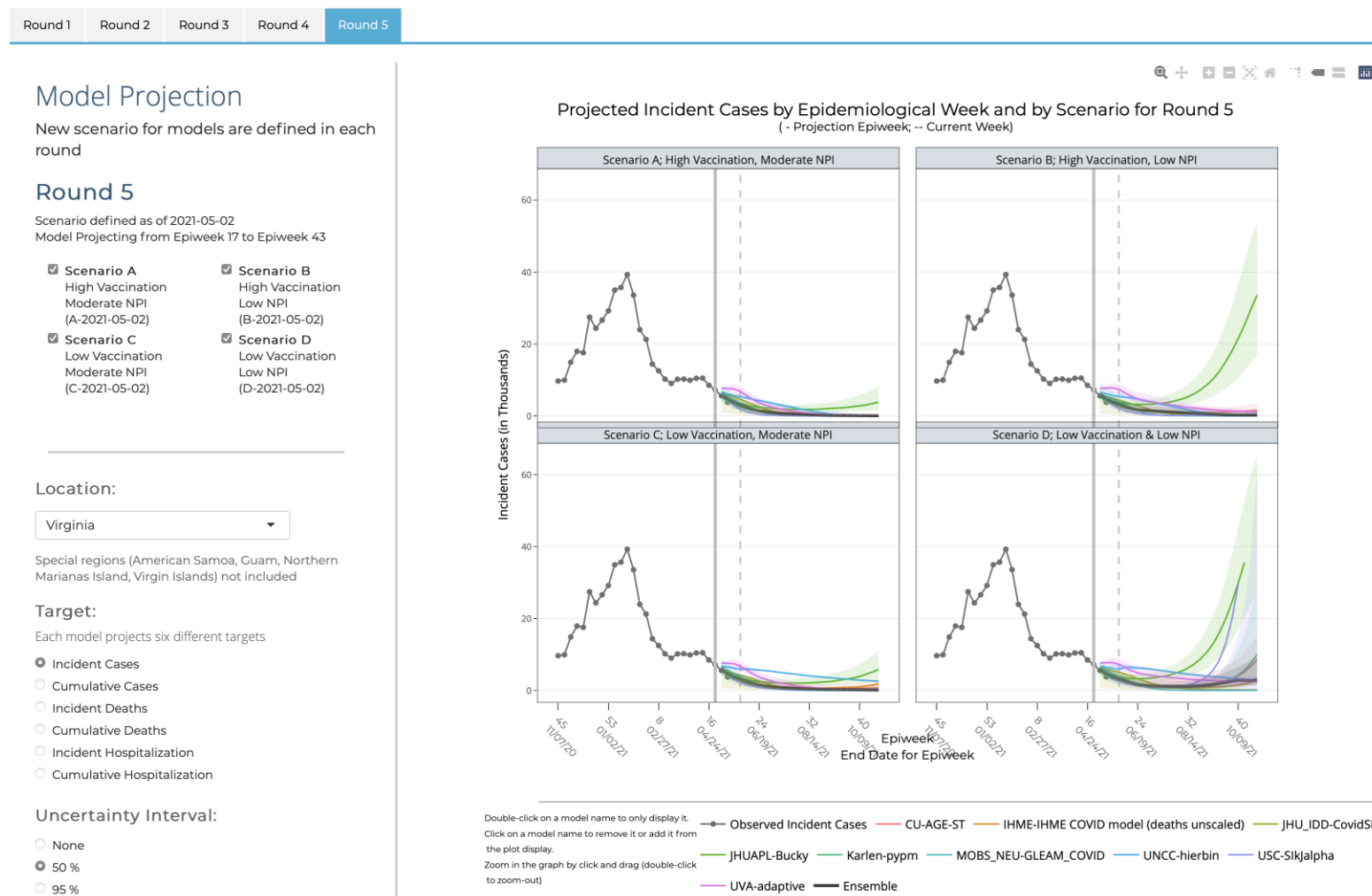
COVID-19 Scenario Modeling Hub

Collaboration of multiple academic teams to provide national and state-by-state level projections for 4 aligned scenarios that vary vaccine rates (high – low) and levels of control (moderate and low)

Round 5 updates now available

Round 4 Results were published May 5th, 2021 in [MMWR](#)

<https://covid19scenariomodelinghub.org/viz.html>



COVID-19 Scenario Modeling Hub – Round 6

Round 6 scenarios explore the effects of a variant similar to the Delta (B.1.617.2) against different backgrounds of vaccination.

Vaccinations by Nov 30

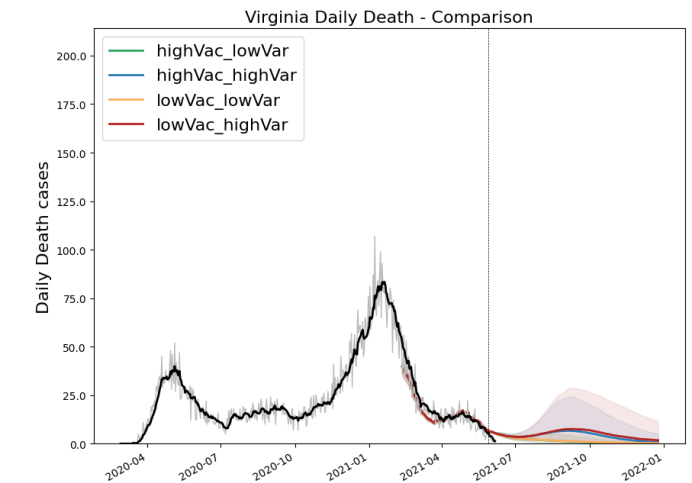
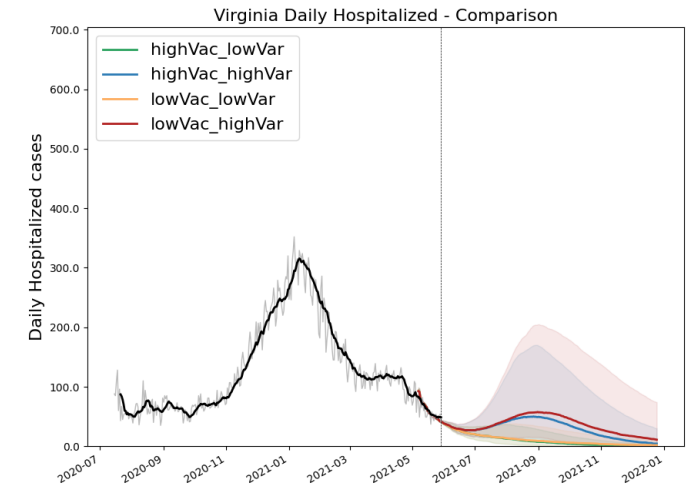
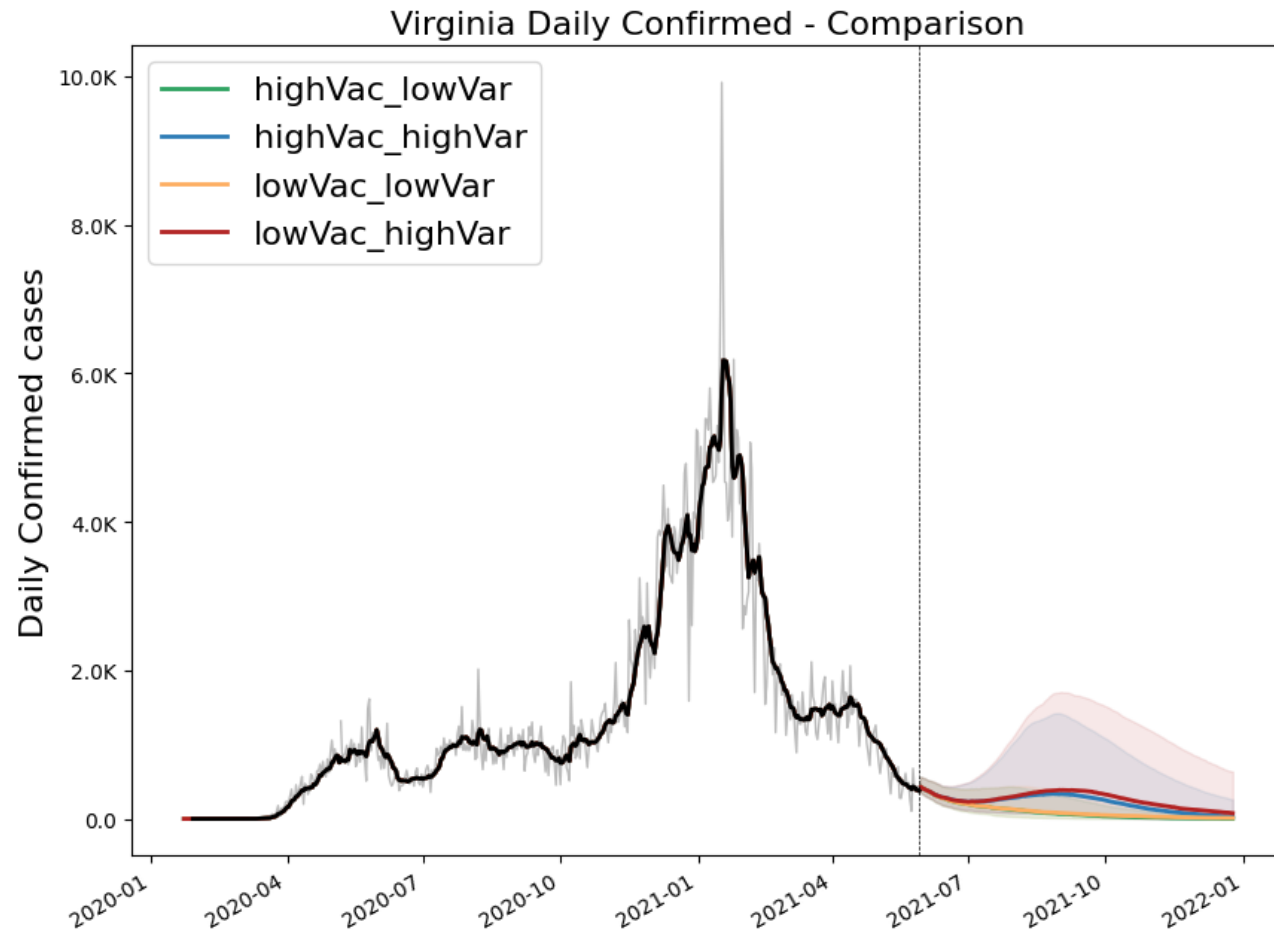
- LowVacc – 68% overall coverage
- HighVacc – 86% overall coverage

Emerging Variant Impact (5% prevalence on May 29th)

- LowVar – 20% more transmissible
- HighVar – 60% more transmissible

	LowVar	HighVar
See more detailed notes for each scenario below	Low Impact Variant (low transmissibility increase, no immune escape)	High Impact Variant (high transmissibility increase, no immune escape)
High Vaccination (Low hesitancy) HighVacc	<p>Scenario A</p> <p>Vaccination:</p> <ul style="list-style-type: none"> - Coverage saturates at 86% nationally among the vaccine-eligible population* by November 30, 2021** - VE is 50%/90% for Pfizer/Moderna against currently circulating variants (1st /2nd dose) - J&J no longer used <p>Variant:</p> <ul style="list-style-type: none"> - 20% increased transmissibility as compared with B.1.1.7 for B.1.617+ variant. 5% prevalence of B.1.617+ nationally on May 29. 	<p>Scenario B</p> <p>Vaccination:</p> <ul style="list-style-type: none"> - Coverage saturates at 86% nationally among the vaccine-eligible population* by November 30, 2021** - VE is 50%/90% for Pfizer/Moderna against currently circulating variants (1st /2nd dose) - J&J no longer used <p>Variant:</p> <ul style="list-style-type: none"> - 60% increased transmissibility as compared with B.1.1.7 for B.1.617+ variant. 5% prevalence of B.1.617+ nationally on May 29.
Low Vaccination (High hesitancy) LowVacc	<p>Scenario C</p> <p>Vaccination:</p> <ul style="list-style-type: none"> - Coverage saturates at 75% nationally among the vaccine-eligible population* by November 30, 2021** - VE is 50%/90% for Pfizer/Moderna against currently circulating variants (1st /2nd dose) and 60% for JJ (1 dose) - J&J no longer used <p>Variant:</p> <ul style="list-style-type: none"> - 20% increased transmissibility as compared with B.1.1.7 for B.1.617+ variant. 5% prevalence of B.1.617+ nationally on May 29. 	<p>Scenario D</p> <p>Vaccination:</p> <ul style="list-style-type: none"> - Coverage saturates at 75% nationally among the vaccine-eligible population* by November 30, 2021** - VE is 50%/90% for Pfizer/Moderna against currently circulating variants (1st /2nd dose) and 60% for JJ (1 dose) - J&J no longer used <p>Variant:</p> <ul style="list-style-type: none"> - 60% increased transmissibility as compared with B.1.1.7 for B.1.617+ variant. 5% prevalence of B.1.617+ nationally on May 29.

Modeling Hub – Round 6 Prelim Results



Key Takeaways

Projecting future cases precisely is impossible and unnecessary.

Even without perfect projections, we can confidently draw conclusions:

- **Case rates in Virginia continue to decline though some districts have small rebounds in rates**
- VA mean weekly incidence down to 2.3/100K from 4/100K, US flattening remaining at 5/100K
- Vaccination rates continue to decline after rebound from 12-16 year-olds
- Forecasts show short-term declining rates across Commonwealth
- CDC coordinated ScenarioHub update shows potential impact of novel variants against different levels of vaccine coverage

The situation continues to change. Models continue to be updated regularly.

References

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NSSAC. PatchSim: Code for simulating the metapopulation SEIR model. <https://github.com/NSSAC/PatchSim>

Virginia Department of Health. COVID-19 in Virginia. <http://www.vdh.virginia.gov/coronavirus/>

Biocomplexity Institute. COVID-19 Surveillance Dashboard. <https://nssac.bii.virginia.edu/covid-19/dashboard/>

Google. COVID-19 community mobility reports. <https://www.google.com/covid19/mobility/>

Biocomplexity page for data and other resources related to COVID-19: <https://covid19.biocomplexity.virginia.edu/>

Questions?

Points of Contact

Bryan Lewis
brylew@virginia.edu

Srini Venkatramanan
srini@virginia.edu

Madhav Marathe
marathe@virginia.edu

Chris Barrett
ChrisBarrett@virginia.edu

Biocomplexity COVID-19 Response Team

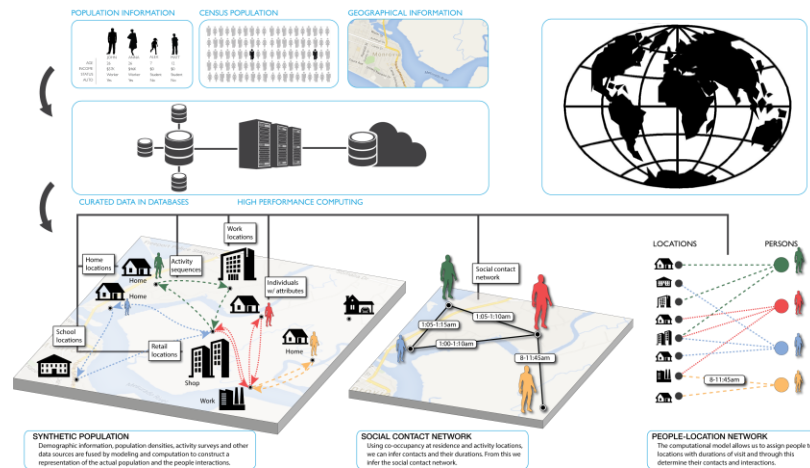
Aniruddha Adiga, Abhijin Adiga, Hannah Baek, Chris Barrett, Golda Barrow, Richard Beckman, Parantapa Bhattacharya, Jiangzhuo Chen, Clark Cucinell, Patrick Corbett, Allan Dickerman, Stephen Eubank, Stefan Hoops, Ben Hurt, Ron Kenyon, Brian Klahn, Bryan Lewis, Dustin Machi, Chunhong Mao, Achla Marathe, Madhav Marathe, Henning Mortveit, Mark Orr, Joseph Outten, Akhil Peddireddy, Przemyslaw Porebski, Erin Raymond, Jose Bayoan Santiago Calderon, James Schlitt, Samarth Swarup, Alex Telionis, Srinivasan Venkatramanan, Anil Vullikanti, James Walke, Andrew Warren, Amanda Wilson, Dawen Xie

Supplemental Slides

Agent-based Model (ABM)

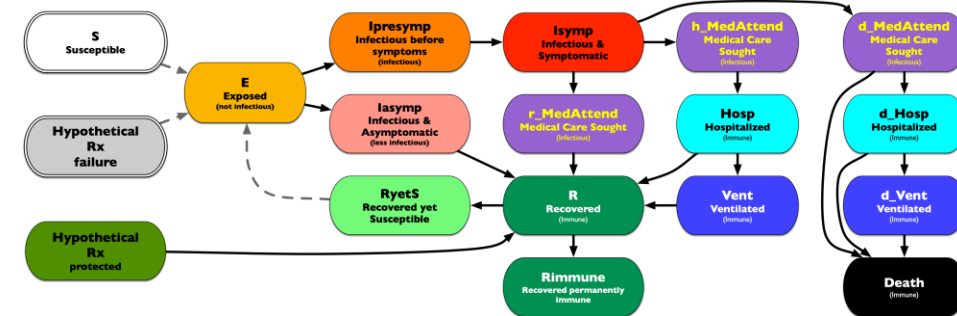
EpiHiper: Distributed network-based stochastic disease transmission simulations

- Assess the impact on transmission under different conditions
- Assess the impacts of contact tracing



Synthetic Population

- Census derived age and household structure
- Time-Use survey driven activities at appropriate locations



Detailed Disease Course of COVID-19

- Literature based probabilities of outcomes with appropriate delays
- Varying levels of infectiousness
- Hypothetical treatments for future developments